

1	Q	I	V	L	T	Q	S	P	A	I	M	S	A	S	P	G	E	K	V	T
1	D	I	Q	M	T	Q	S	P	S	T	L	S	A	S	V	G	D	R	V	T
21	I	T	C	S	A	S	S	S	I		S	Y	M	H	W	F	Q	K	P	
21	I	T	C	R	A	S	Q	S	I	N	T	W	L	A	W	Y	Q	Q	K	P
40	G	T	S	P	K	L	W	I	Y	T	T	S	N	L	A	S	G	V	P	A
41	G	K	A	P	K	L	L	<u>M</u>	Y	K	A	S	S	L	E	S	G	V	P	<u>S</u>
60	R	F	S	G	S	G	S	G	T	S	Y	S	L	T	I	S	R	M	E	A
61	R	F	<u>I</u>	G	S	G	S	G	T	E	F	T	L	T	I	S	S	L	Q	P
80	E	D	A	A	T	Y	Y	C	H	Q	R	S	T	Y	P	L	T	F	G	S
81	D	D	F	A	T	Y	Y	C	Q	Q	Y	N	S	D	S	K	M	F	G	Q
100	G	T	K	L	E	L	K													
101	G	T	K	V	E	V	K													

FIGURE 1A

1	Q	V	Q	L	Q	Q	S	G	A	E	L	A	K	P	G	A	S	V	K	M
1	Q	V	Q	L	V	Q	S	G	A	E	V	K	K	P	G	S	S	V	K	V
21	S	C	K	A	S	G	Y	T	F	T	S	Y	R	M	H	W	V	K	Q	R
21	S	C	K	A	S	G	<u>G</u>	T	F	<u>S</u>	R	S	A	I	I	W	V	R	Q	A
41	P	G	Q	G	L	E	W	I	G	Y	I	N	P	S	T	G	Y	T	E	Y
41	P	G	Q	G	L	E	W	<u>M</u>	G	G	I	V	P	M	F	G	P	P	N	Y
61	N	Q	K	F	K	D	K	A	T	L	T	A	D	K	S	S	S	T	A	Y
61	A	Q	K	F	Q	G	<u>R</u>	<u>V</u>	T	I	T	A	D	E	S	T	N	T	A	Y
81	M	Q	L	S	S	L	T	F	E	D	S	A	V	Y	Y	C	A	R	G	
81	M	E	L	S	S	L	R	S	E	D	T	A	<u>F</u>	Y	<u>F</u>	C	A	<u>G</u>	<u>G</u>	Y
100	G	G	V	F	D	Y	W	G	Q	G	T	T	L	T	V	S	S	S		
101	G	I	Y	S	P	E	<u>E</u>	<u>Y</u>	<u>N</u>	G	<u>G</u>	L	V	T	V	S	S	S		

FIGURE 1B

1	D	I	V	L	T	Q	S	P	<u>A</u>	S	L	A	V	S	L	G	Q	R	A	T
1	E	I	V	M	T	Q	S	P	<u>A</u>	T	L	S	V	S	P	G	E	R	A	T
21	I	S	C	R	A	S	Q	S	V	S	T	S	T	Y	N	Y	M	H	W	Y
21	L	S	C	<u>R</u>	<u>A</u>	S	Q	S	V	S	T	S	T	Y	N	Y	M	H	W	Y
41	Q	Q	K	P	G	Q	P	P	K	L	L	I	K	Y	A	S	N	L	E	S
41	Q	Q	K	P	<u>G</u>	<u>Q</u>	S	P	R	L	L	I	<u>K</u>	<u>Y</u>	A	S	N	L	E	S
61	G	V	P	A	R	F	S	G	S	G	F	G	T	D	F	T	L	N	I	H
61	G	I	P	A	R	F	S	G	S	G	S	G	T	E	F	T	L	T	I	S
81	P	V	E	E	E	D	T	V	T	Y	Y	C	Q	H	S	W	E	I	P	Y
81	<u>R</u>	<u>L</u>	<u>E</u>	<u>S</u>	<u>E</u>	<u>D</u>	<u>F</u>	<u>A</u>	<u>V</u>	<u>Y</u>	<u>Y</u>	<u>C</u>	<u>Q</u>	<u>H</u>	<u>S</u>	<u>W</u>	<u>E</u>	<u>I</u>	<u>P</u>	<u>Y</u>
101	T	F	G	G	G	T	K	L	E	I	K									
101	T	F	G	Q	G	T	R	V	E	I	K									

FIGURE 2A

1	E	M	I	L	V	E	S	G	G	G	L	V	K	P	G	A	S	L	K	L
1	E	V	Q	L	L	E	S	G	G	G	L	V	Q	P	G	G	S	L	R	L
21	S	C	A	A	S	G	F	T	F	S	N	Y	G	L	S	W	V	R	Q	T
21	S	C	A	A	S	G	F	T	F	S	<u>N</u>	Y	<u>G</u>	<u>L</u>	<u>S</u>	<u>W</u>	<u>V</u>	<u>R</u>	<u>Q</u>	A
41	S	D	R	R	L	E	W	V	A	S	I	S	R	G	G	G	R	I	Y	S
41	P	G	K	G	L	E	W	V	A	<u>S</u>	I	S	R	G	G	G	R	I	Y	S
61	P	D	N	L	K	G	R	F	T	I	S	R	E	D	A	K	N	T	L	Y
61	P	D	N	L	K	<u>G</u>	R	F	T	I	S	R	N	D	S	K	N	T	L	Y
81	L	Q	M	S	S	L	K	S	E	D	T	A	L	Y	Y	C	L	R	E	G
81	L	<u>Q</u>	M	N	S	L	Q	A	E	D	T	A	L	Y	Y	C	<u>L</u>	R	<u>E</u>	G
101	I	Y	Y	A	D	Y	G	F	F	D	V	W	G	T	G	T	T	V	I	V
101	I	Y	Y	A	D	Y	G	F	F	D	V	<u>W</u>	G	Q	G	T	L	V	T	V
121	S	S																		
121	S	S																		

FIGURE 2B

1	D	I	V	M	T	Q	S	H	K	F	M	S	T	S	V	G	D	R	V	S
1	D	I	Q	M	T	Q	S	P	S	T	L	S	A	S	V	G	D	R	V	T
21	I	T	C	K	A	S	Q	D	V	G	S	A	V	V	W	H	Q	Q	K	S
21	I	T	C	<u>K</u>	A	S	Q	D	V	G	S	A	V	V	W	<u>H</u>	Q	Q	K	P
41	G	Q	S	P	K	L	L	I	Y	W	A	S	T	R	H	T	G	V	P	D
41	G	K	A	P	<u>K</u>	L	L	<u>I</u>	Y	<u>W</u>	A	S	T	R	H	T	G	V	P	S
61	R	F	T	G	S	G	S	G	T	D	F	T	L	T	I	T	N	V	Q	S
61	R	F	<u>T</u>	G	S	G	S	G	T	E	F	T	L	T	I	S	S	L	Q	P
81	E	D	L	A	D	Y	F	C	Q	Q	Y	S	I	F	P	L	T	F	G	A
81	D	D	F	A	T	Y	<u>F</u>	C	<u>Q</u>	<u>Q</u>	Y	S	I	F	P	L	T	F	G	Q
101	G	T	R	L	E	L	K													
101	G	T	K	V	E	V	K													

FIGURE 3A

1	Q	V	Q	L	Q	Q	S	D	A	E	L	V	K	P	G	A	S	S	V	K	I
1	Q	V	Q	L	V	Q	S	G	A	E	V	K	K	P	G	S	S	V	K	V	
21	S	C	K	V	S	G	Y	T	F	T	D	H	T	I	H	W	M	K	Q	R	
21	S	C	K	A	S	G	<u>Y</u>	T	F	<u>T</u>	D	H	T	I	H	W	<u>M</u>	R	Q	A	
41	P	E	Q	G	L	E	W	F	G	Y	I	Y	P	R	D	G	H	T	R	Y	
41	P	G	Q	G	L	E	W	<u>F</u>	G	<u>Y</u>	I	Y	P	R	D	G	H	T	R	Y	
61	S	E	K	F	K	G	K	A	T	L	T	A	D	K	S	A	S	T	A	Y	
61	<u>A</u>	E	K	F	K	G	<u>K</u>	<u>A</u>	T	I	T	A	D	E	S	T	N	T	A	Y	
81	M	H	L	N	S	L	T	S	E	D	S	A	V	Y	F	C	A	R	G	R	
81	M	E	L	S	S	L	R	S	E	D	T	A	<u>V</u>	Y	F	C	A	<u>R</u>	<u>G</u>	R	
101	D	S	R	E	R	N	G	F	A	Y	W	G	Q	G	T	L	V	T	V	S	
101	D	S	R	E	R	N	G	F	A	Y	<u>W</u>	<u>G</u>	<u>Q</u>	<u>G</u>	<u>T</u>	L	V	T	V	S	
121	A																				
121	S																				

FIGURE 3B

1	D	I	V	L	T	Q	S	P	A	S	L	A	V	S	L	G	Q	R	A	T
1	D	I	Q	M	T	Q	S	P	S	<u>S</u>	L	S	A	S	V	G	D	R	V	T
21	I	S	C	R	A	S	E	S	V	D	N	Y	G	I	S	F	M	N	W	F
21	I	T	C	<u>R</u>	A	S	E	S	V	D	N	Y	G	I	S	F	M	N	W	<u>F</u>
41	Q	Q	K	P	G	Q	P	P	K	L	L	I	Y	A	A	S	N	Q	G	S
41	Q	Q	K	P	G	K	A	P	K	L	L	<u>I</u>	Y	<u>A</u>	<u>A</u>	S	N	Q	G	S
61	G	V	P	A	R	F	S	G	S	G	S	G	T	D	F	S	L	N	I	H
61	G	V	P	S	R	F	<u>S</u>	G	S	G	S	G	T	<u>D</u>	F	T	L	N	I	S
81	P	M	E	E	D	D	T	A	M	Y	F	C	Q	Q	S	K	E	V	P	W
81	S	L	Q	P	D	D	F	A	T	Y	Y	C	<u>Q</u>	<u>Q</u>	S	K	E	V	P	W
101	T	F	G	G	G	T	K	L	E	I	K									
101	<u>T</u>	F	G	Q	G	T	K	V	E	<u>I</u>	K									

FIGURE 4A

1	E	V	Q	L	Q	Q	S	G	P	E	L	V	K	P	G	A	S	V	K	I
1	Q	V	Q	L	V	Q	S	G	A	E	V	K	K	P	G	S	S	V	K	V
21	S	C	K	A	S	G	Y	T	F	T	D	Y	N	M	H	W	V	K	Q	S
21	S	C	K	A	S	G	<u>Y</u>	T	F	<u>T</u>	D	Y	N	M	H	W	V	R	Q	A
41	H	G	K	S	L	E	W	I	G	Y	I	Y	P	Y	N	G	G	T	G	Y
41	P	G	Q	G	L	E	W	<u>I</u>	G	<u>Y</u>	I	Y	P	Y	N	G	G	T	G	Y
61	N	Q	K	F	K	S	K	A	T	L	T	V	D	N	S	S	S	T	A	Y
61	<u>N</u>	O	K	F	K	S	<u>K</u>	<u>A</u>	T	I	T	A	D	E	S	T	N	T	A	Y
81	M	D	V	R	S	L	T	S	E	D	S	A	V	Y	Y	C	A	R	G	R
81	M	E	L	S	S	L	R	S	E	D	T	A	<u>V</u>	<u>Y</u>	<u>Y</u>	C	A	<u>R</u>	G	R
101	P	A	M	D	Y	W	G	Q	G	T	S	V	T	V	S	S				
101	P	A	M	D	Y	<u>W</u>	<u>G</u>	<u>Q</u>	<u>G</u>	<u>T</u>	L	V	T	V	S	S				

FIGURE 4B

1	Q	I	V	L	T	Q	S	P	A	I	M	S	<u>A</u>	S	P	G	E	K	V	T
1	D	I	Q	M	T	Q	S	P	S	S	L	S	<u>A</u>	S	V	G	D	R	V	T
21	M	T	C	S	G	S	S	S	V	S	F	M	Y	W	Y	Q	Q	R	P	G
21	I	T	C	<u>S</u>	<u>G</u>	<u>S</u>	<u>S</u>	<u>S</u>	V	S	F	M	Y	W	Y	Q	Q	K	P	G
41	S	S	P	R	L	L	I	Y	D	T	S	N	L	A	S	G	V	P	V	R
41	<u>K</u>	A	P	K	L	L	I	Y	<u>D</u>	<u>T</u>	<u>S</u>	<u>N</u>	<u>L</u>	<u>A</u>	<u>S</u>	<u>G</u>	V	P	S	R
61	F	S	G	S	G	S	G	T	S	Y	S	L	T	I	S	R	M	E	A	E
61	F	S	G	S	G	S	G	T	D	<u>Y</u>	T	F	T	I	S	S	L	Q	P	E
81	D	A	A	T	Y	Y	C	Q	Q	W	S	T	Y	P	L	T	F	G	A	G
81	D	I	A	T	Y	Y	C	<u>Q</u>	<u>Q</u>	<u>W</u>	<u>S</u>	<u>T</u>	<u>Y</u>	<u>P</u>	<u>L</u>	<u>T</u>	<u>F</u>	<u>G</u>	<u>Q</u>	<u>G</u>
101	T	K	L	E	L	K														
101	T	K	V	E	V	K														

FIGURE 5A

1	Q	V	Q	L	K	Q	S	G	P	G	L	V	Q	P	S	Q	S	L	S	I
1	<u>E</u>	V	Q	L	L	E	S	G	G	G	L	V	Q	P	G	Q	S	L	R	L
21	T	C	T	V	S	G	F	S	V	T	S	Y	G	V	H	W	I	R	Q	S
21	S	C	A	A	S	G	F	T	<u>V</u>	<u>T</u>	<u>S</u>	<u>Y</u>	<u>G</u>	<u>V</u>	<u>H</u>	<u>W</u>	<u>V</u>	<u>R</u>	<u>Q</u>	<u>A</u>
41	P	G	K	G	L	E	W	L	G	V	I	W	S	G	G	S	T	D	Y	N
41	P	G	K	G	L	E	W	V	<u>G</u>	<u>V</u>	<u>I</u>	<u>W</u>	<u>S</u>	<u>G</u>	<u>G</u>	<u>S</u>	<u>T</u>	<u>D</u>	<u>Y</u>	<u>N</u>
61	A	A	F	I	S	R	L	T	I	S	K	D	N	S	K	S	Q	V	F	F
61	<u>A</u>	<u>A</u>	<u>F</u>	<u>I</u>	<u>S</u>	<u>R</u>	<u>F</u>	<u>T</u>	<u>I</u>	<u>S</u>	<u>R</u>	<u>D</u>	<u>N</u>	<u>S</u>	<u>K</u>	<u>N</u>	<u>T</u>	<u>L</u>	<u>Y</u>	<u>L</u>
81	K	V	N	S	L	Q	P	A	D	T	A	I	Y	Y	C	A	R	A	G	D
81	Q	M	N	<u>S</u>	L	Q	A	E	<u>D</u>	<u>T</u>	A	I	Y	Y	C	A	R	<u>A</u>	<u>G</u>	D
101	Y	N	Y	D	G	F	A	Y	W	G	Q	G	T	L	V	T	V	S	A	
101	Y	N	Y	D	G	F	A	Y	W	G	Q	G	T	L	V	T	V	S	S	

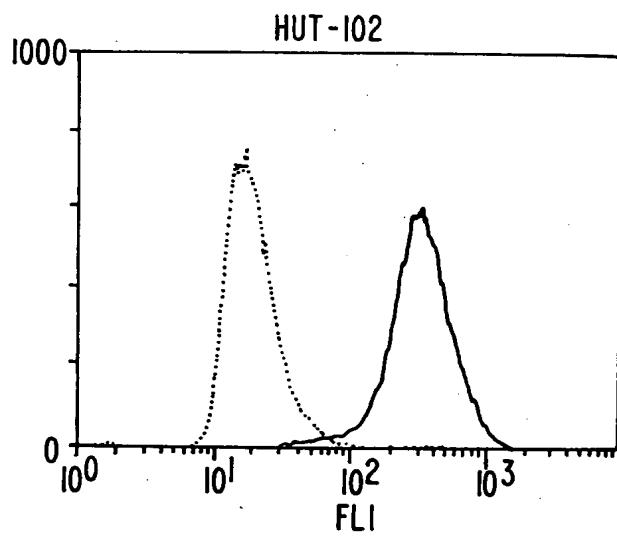
FIGURE 5B

1	D	I	V	L	T	Q	S	P	A	T	L	S	V	T	P	G	D	S	V	S
1	E	I	V	L	T	Q	S	P	G	T	L	S	L	S	P	G	E	R	A	T
21	L	S	C	R	A	S	Q	S	I	S	N	N	L	H	W	Y	Q	Q	K	S
21	L	S	C	<u>R</u>	A	S	Q	S	I	S	N	N	L	H	W	Y	Q	Q	K	P
41	H	E	S	P	R	L	L	I	K	Y	A	S	Q	S	I	S	G	I	P	S
41	G	Q	A	P	R	L	L	I	<u>K</u>	Y	A	S	Q	S	I	S	G	I	P	D
61	R	F	S	G	S	G	S	G	T	D	F	T	L	S	V	N	G	V	E	T
61	R	F	S	G	S	G	S	G	T	D	F	T	L	T	I	S	R	L	E	P
81	E	D	F	G	M	Y	F	C	Q	Q	S	N	S	W	P	H	T	F	G	G
81	E	D	F	A	V	Y	Y	C	<u>Q</u>	<u>Q</u>	S	N	S	W	P	H	T	F	G	Q
101	G	T	K	L	E	I	K													
101	G	T	K	V	E	I	K													

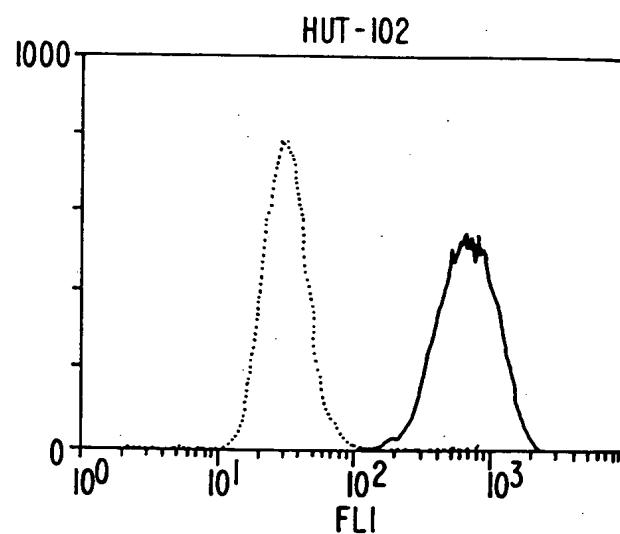
FIGURE 6A

1	E	V	Q	L	<u>Q</u>	Q	S	G	P	E	L	V	K	K	P	G	A	S	M	K	I
1	Q	V	Q	L	<u>V</u>	Q	S	G	A	E	V	K	K	P	G	S	S	V	R	V	
21	S	C	K	A	S	V	Y	S	F	T	G	Y	T	M	N	W	V	K	Q	S	
21	S	C	K	<u>A</u>	S	G	<u>Y</u>	S	<u>F</u>	<u>T</u>	G	Y	T	M	N	W	V	R	Q	A	
41	H	G	Q	N	L	E	W	I	G	L	I	N	P	Y	N	G	G	T	S	Y	
41	P	G	K	G	L	E	W	V	G	<u>L</u>	I	N	P	Y	N	G	G	T	S	Y	
61	N	Q	K	F	K	G	K	A	T	L	T	V	D	K	S	S	N	T	A	Y	
61	N	Q	K	F	K	G	R	V	<u>T</u>	V	S	L	K	P	S	F	N	Q	A	<u>Y</u>	
81	M	E	L	L	S	L	T	S	A	D	S	A	V	Y	Y	C	T	R	R	G	
81	M	E	L	S	S	L	F	S	E	D	T	A	V	Y	Y	C	<u>T</u>	R	R	G	
101	F	R	D	Y	S	M	D	Y	W	G	Q	G	T	S	V	T	V	S	S	S	
101	F	R	D	Y	S	M	D	Y	W	G	Q	G	T	L	V	T	V	S	S	S	

FIGURE 6B



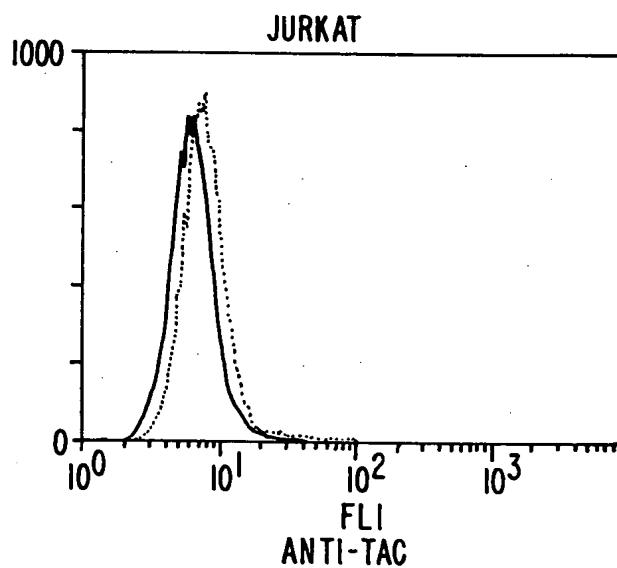
HUMANIZED ANTI-TAC



ANTI-TAC

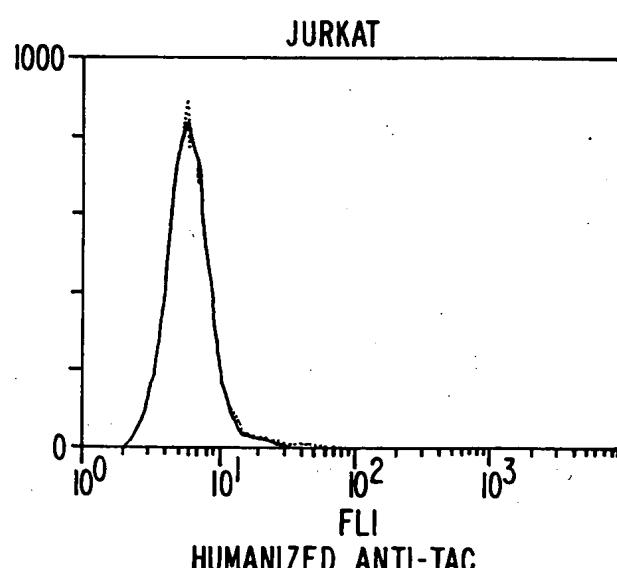
FIGURE 7A

FIGURE 7B



ANTI-TAC

FIGURE 7C



HUMANIZED ANTI-TAC

FIGURE 7D

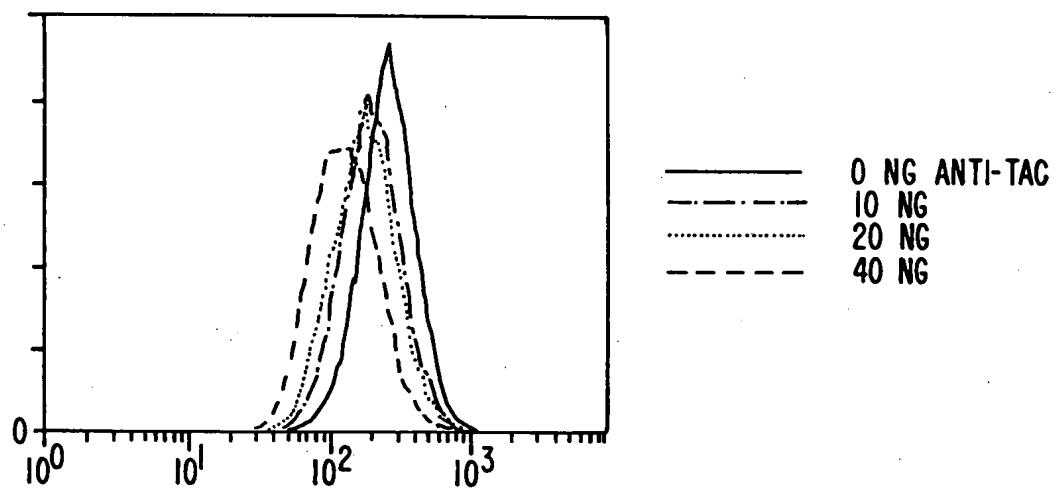


FIGURE 8A

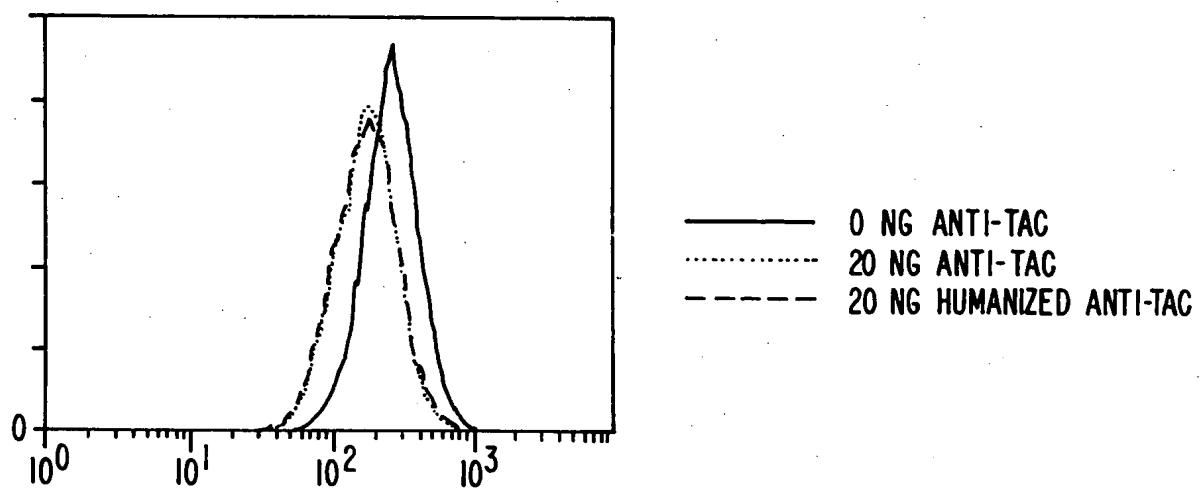


FIGURE 8B

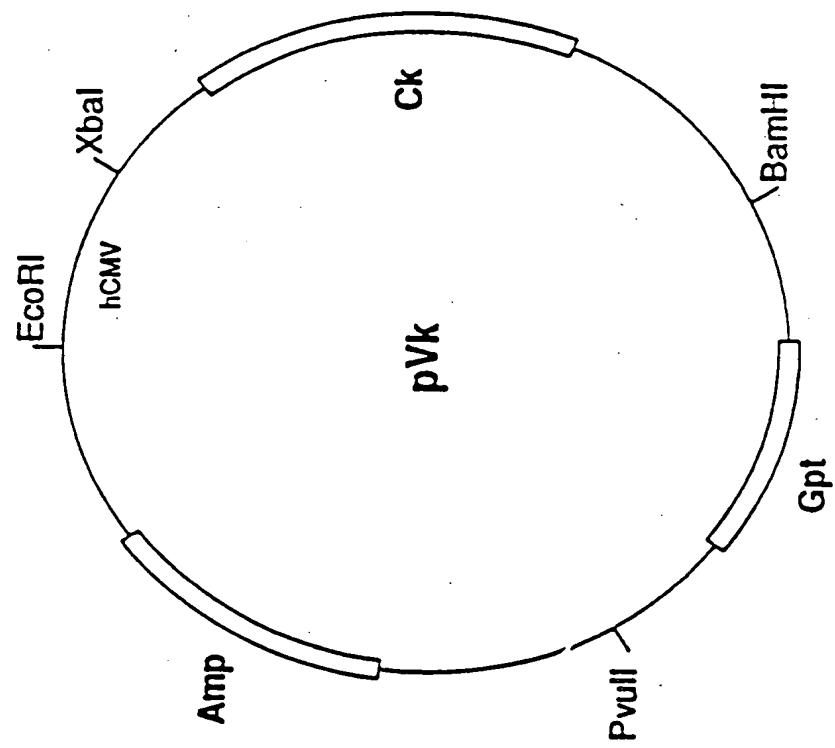


FIGURE 9B

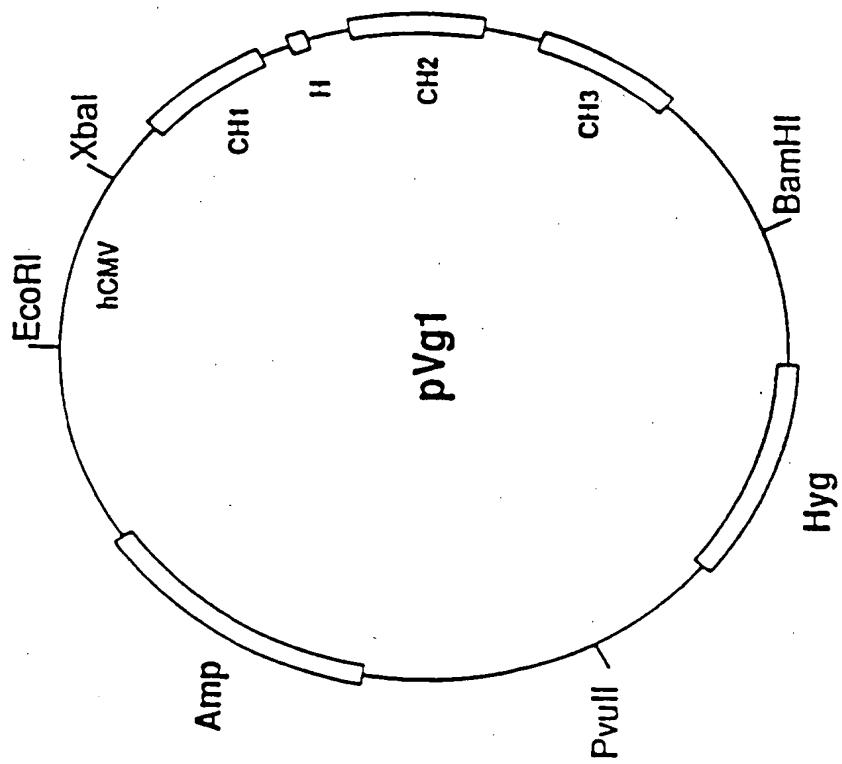


FIGURE 9A

FIGURE 10A

FIGURE 10B

10	20	30	40	50	60	70
AGCTTCTAGA	TGGGATGGAG	CTGGATCTTT	CTCTTCCCTCC	TGTCAGGTA	CGGGGGGTG	CACTCTCAGG
<u>TCGAAGATCT</u>	<u>ACCCCTACCTC</u>	<u>GACCTAGAAA</u>	<u>GAGAAGGAGG</u>	<u>ACAGTCCATG</u>	<u>GGCCCCCAC</u>	<u>CTGAAGAGTCC</u>
80	90	100	110	120	130	140
TCCAGGCTGT	CCAGTCTGGG	GCTGAAGTCA	AGAAACCTGG	CTCGAGGGTG	AAGGTCTCCT	CCAAGGGCTC
<u>AGGTCGAACA</u>	<u>GGTCAGACCC</u>	<u>CGACTTCAGT</u>	<u>TCTTGGACC</u>	<u>GACCTGCCAC</u>	<u>TICCAAGAGGA</u>	<u>CGTTCGGAG</u>
150	160	170	180	190	200	210
TGGCCGGACC	TTTTCTAGCT	ACAGGATGCC	CTGGCTTAAGC	CAGGCCCCCTG	CACAGGGCTCT	CGAATGGATG
<u>ACGGCCCTGG</u>	<u>AAAAGATCGA</u>	<u>TGTCCCTACGT</u>	<u>GACCCATTC</u>	<u>GTCGGGGAC</u>	<u>CTGTCGCCAGA</u>	<u>CCTTAACCTAC</u>
220	230	240	250	260	270	280
GGATATATA	ATCCCTCGAC	TGGGTATACT	GAATACATC	AGAAATTCA	GGACAGGGTC	ACAATTACTG
<u>CCTATATAAT</u>	<u>TAGGCCAGCTG</u>	<u>ACCCATATGA</u>	<u>CTTATGTTAG</u>	<u>TCTTCAAGTT</u>	<u>CTGTCCAG</u>	<u>TGTTAATGAC</u>
290	300	310	320	330	340	350
CAGACGAATC	CACCAATAACA	GCCTACATGG	AACTGAGGAG	CCTGAGATCT	GAGGACACCG	CATTCTATT
<u>CTCTGGCTAG</u>	<u>GTGGTTATGT</u>	<u>CGGATGTTAC</u>	<u>TTGACTCTGTC</u>	<u>GOACTCTAGA</u>	<u>CTCCTGTGCC</u>	<u>GTAAGATAAA</u>
360	370	380	390	400	410	420
CTCTGGCAAGG	GGTGGGGAG	TCTTGTACTA	CGAATAACAT	CGAGGGCTG	TCACAGTCTC	CTCAGGTGAG
<u>GACACCTCCC</u>	<u>CCACCCCTTC</u>	<u>AGAAACTGAT</u>	<u>GCTTATGTTA</u>	<u>CCTCCCGAC</u>	<u>AGTGTAGAG</u>	<u>GAGTCCACTC</u>
430	440					
TCCTTAAAC	CTCTAGACCA	TAT				
<u>AGGAATTTC</u>	<u>GAGATCTGCT</u>	<u>ATA</u>				

FIGURE 11A

10 20 30 40 50 60 70
CAAATCTAGA TGGAGACCGA TACCCCTCCTG CTATGGTCC TCTGGTATG GGTCCAGGA TCAACGGAG
GTTTAGATCT ACTCTGGCT ATGGAGGAC GATACCCAGG AGGACGATAAC CCAGGGTCT AGTTGGCCT

 80 90 100 110 120 130 140
ATATTCACT GACCCAGTCT CCATCTACCC TCTCTGGCTAG CGTCGGGGAT AGGGTCACCA TAACCTGCTC
TATAAGTCTA CTGGGTCAAG GGTAGATGGG AGAGACGATC CCAGGCCCTA TCCCACTGTT ATGGACGAG

 150 160 170 180 190 200 210
TCCCAGGTCA AGTATAAGT ACATGCCACTG GTACCCAGCAG AAGCCAGGCC AAGCTCCAA GCTTCTAATG
ACGGTCCAGT TCAATTCAA TGTACCTCAC CATGGTCGTC TTGGGTCCGT TTGGAGGGTT CGAACGATTAC

 220 230 240 250 260 270 280
TATACCACT CCAACCTGGC TTCTGGAGTC CCTTCTCGCT TCATTGGCAG TGGATCTGGG ACCGAGTTCA
ATATGGTCA GCTTGGACCC AAGACCTCAG GGAAGAACGGA AGTAACCGTC ACCTAGACCC TGGCTCAAGT

 290 300 310 320 330 340 350
CCCTCACAA T CAGCTCTCTG CAGCCAGATG ATTCGGCAC TTATTACTGC CATCAAAGGA GTACTTACCC
GGGACTGTTA GTGGAGAGAC GTCGGTCTAC TAAAGCCGTG AATAATGACG GTAGTTTCCT CATGAAATGGC

 360 370 380 390 400
ACTCACCGTC GGTCAAGGGGA CCAACGGGA GGTCAAAACGT AACTACACTT TTCTAGATAT A
TGAGTGCAG CCAGTCCCCCT GGTTCACCT CCAGTTGCA TTCATGTGA AAGATCTATA T

FIGURE 11B

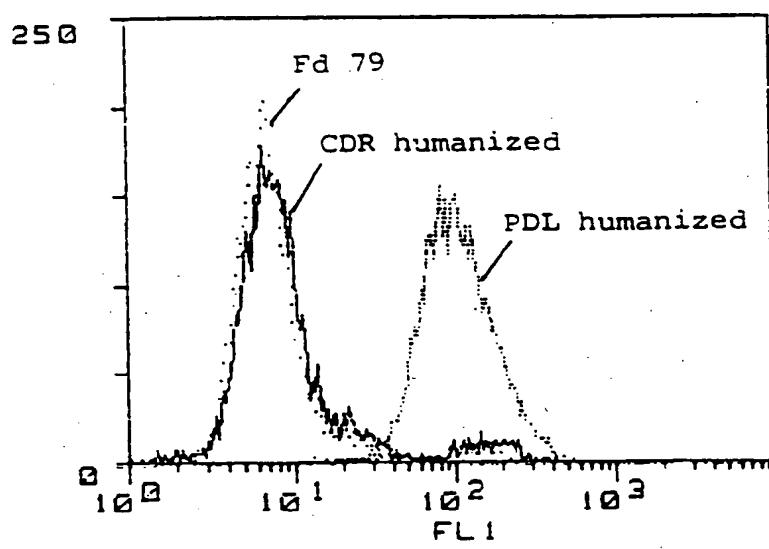


FIGURE 12

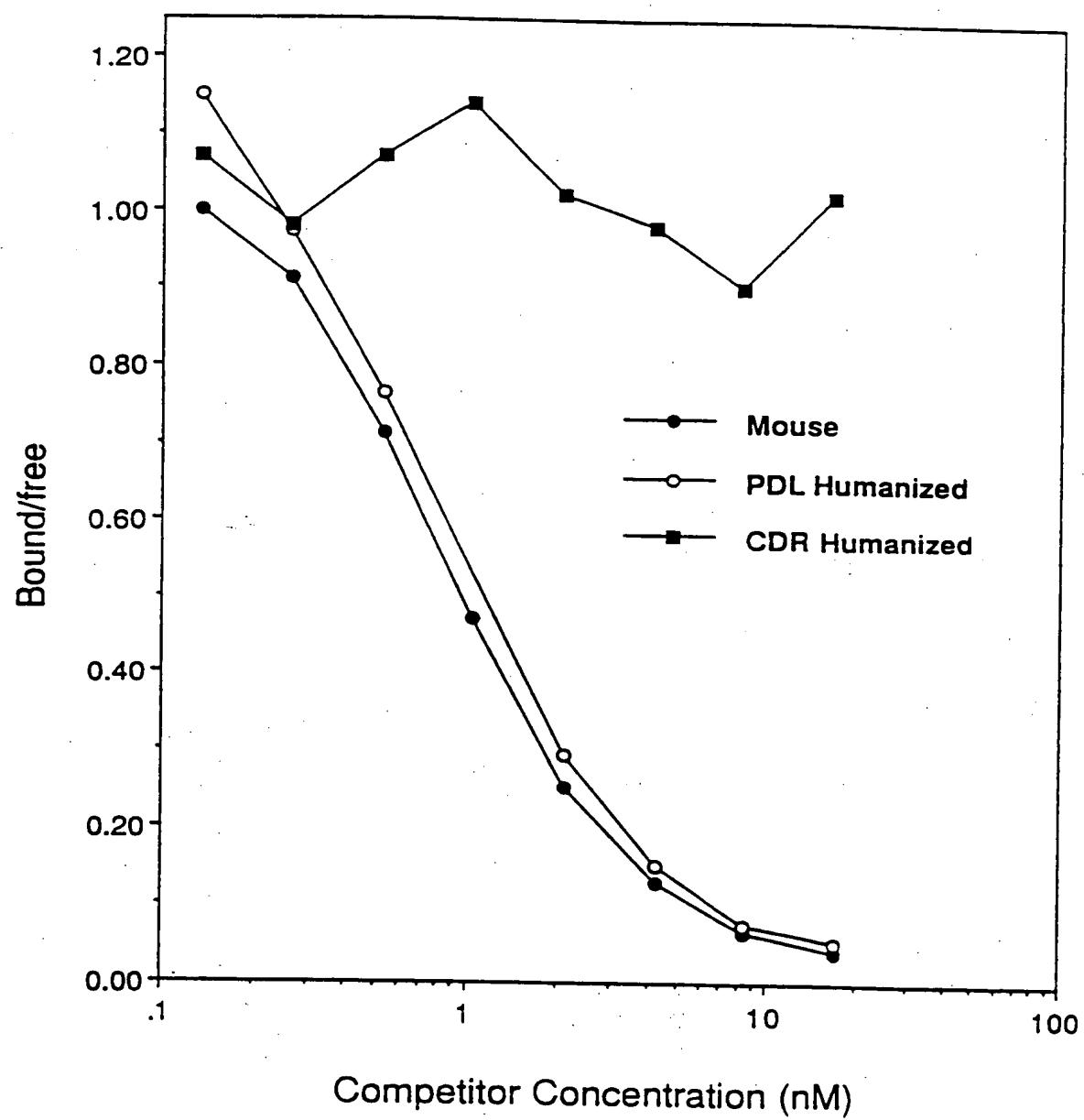


FIGURE 13

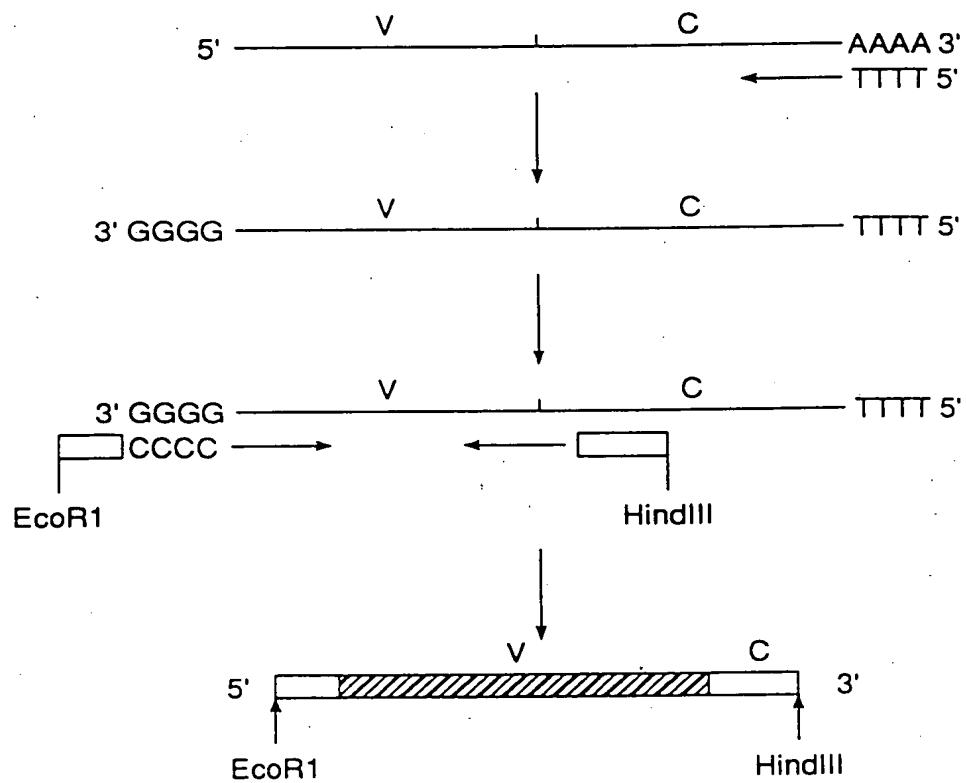


FIGURE 14

1	0 Y 0 L 0 0 S G A E L A K P G A S Y K M
1	0 Y 0 L V 0 S G A E V K K P G S S V K V
21	S C K A S G Y T F T S Y R M H W V K Q R
21	S C K A S G G T F S R S A I I W V R Q A
41	P G 0 G L E W I G Y I N P S T G Y T E Y
41	P G 0 G L E W I M G G V P M F G P P N Y
61	N 0 K F K D K A T L T A D K S S T A Y
61	A Q K F Q G R V T I T A D E S T N T A Y
81	M 0 L S S I T F E D S A V Y Y C A R G
81	M E L S S L R S E D T A F Y F C A G G Y
100	G G V F D Y W G O G T T L T V S S
101	G I Y S P E E Y N G L V T V S S

FIGURE 15

1	0	1	V	L	T	0	S	P	A	1	M	S	A	S	P	G	E	K	V	T	
1	D	1	O	M	T	0	S	P	S	T	L	S	A	S	V	G	D	R	V	T	
21	1	1	T	C	S	A	S	S	S	1	N	T	W	L	A	W	Y	0	0	K	P
21	1	1	T	C	R	A	S	0	S	1	N	T	W	L	A	W	Y	0	0	K	P
40	6	T	S	P	K	L	W	1	Y	T	T	S	N	L	A	S	G	V	P	A	
41	6	K	A	P	K	L	L	M	Y	K	A	S	S	L	E	S	G	V	P	S	
60	8	F	S	G	S	G	S	G	T	S	Y	S	L	T	T	S	R	M	E	A	
61	8	F	1	G	S	G	S	G	T	E	F	T	L	T	T	S	S	L	O	P	
80	8	D	A	A	T	Y	Y	C	H	Q	R	S	T	Y	P	L	T	F	G	S	
81	8	D	D	F	A	T	Y	Y	C	0	0	Y	N	S	D	S	K	M	F	G	
100	6	T	K	L	E	L	K														
101	6	T	K	V	E	V	K														

FIGURE 16

10 20 30 40 50 60
 TCTAGATGGATGGAGCTGGATCTTCTCTCCTGTCAGGTACCGCGGGCGTGCACT
 M G W S W I F L F L L S G T A G V H

 70 80 90 100 110 120
 CTCAGGTCCAGCTTGTCAGTCTGGGCTGAAGTCAAGAACCTGGCTCGAGCGTGAAGG
 S Q V Q L V Q S G A E V K K P G S S V K

 130 140 150 160 170 180
 TCTCCTGCAAGGCTTCTGGCTACACCTTTACTAGCTACAGGATGCACTGGTAAGGCAGG
 V S C K A S G Y T F T S Y R M H W V R Q

 190 200 210 220 230 240
 CCCCTGGACAGGGTCTGGAATGGATTGGATATATTAAATCCGTGACTGGGTATACTGAAT
 A P G Q G L E W I G Y I N P S T G Y T E

 250 260 270 280 290 300
 ACAATCAGAAGTTCAAGGACAAGGCAACAATTACTGCAGACGAATCCACCAATAAGCCT
 Y N Q K F K D K A T I T A D E S T N T A

 310 320 330 340 350 360
 ACATGGAACTGAGCAGCCTGAGATCTGAGGACACCGCAGTCTATTACTGTGCAAGAGGGG
 Y M E L S S L R S E D T A V Y Y C A R G

 370 380 390 400 410 420
 GGGGGGTCTTGAATCTGGGGCCAAGGAACCTGGTACAGTCTCCTCAGGTGAGTCCT
 G G V F D Y W G Q G T L V T V S S

 430
 TAAAACCTCTAGA

FIGURE 17

10 20 30 40 50 60
 TCTAGATGGAGACCGATACCCTCCTGCTATGGGTCCCTGCTATGGGTCCCAGGATCAA
 M E T D T L L W V L L W V P G S
 70 80 90 100 110 120
 CCGGAGATATTAGATGACCCAGTCTCCATCTACCCCTCTCTGCTAGCGTCGGGGATAGGG
 T G D I Q M T Q S P S T L S A S V G D R
 130 140 150 160 170 180
 TCACCATAACCTGCTCTGCCAGCTCAAGTATAAGTTACATGCACCTGGTACCAAGCAGAAC
 V T I T C S A S S S I S Y M H W Y Q Q K
 190 200 210 220 230 240
 CAGGCCAAAGCTCCCAAGCTTCTAATTATACCAACATCCAACCTGGCTTCTGGAGTCCCTG
 P G K A P K L L I Y T T S N L A S G V P
 250 260 270 280 290 300
 CTCGCTTCAGTGGCAGTGGATCTGGGACCGAGTTCACCTCACAAATCAGCTCTCTGCAGC
 A R F S G S G S G T E F T L T I S S L Q
 310 320 330 340 350 360
 CAGATGATTTGCCACTTATTACTGCCATCAAAGGAGTACTTACCCACTCACGTTGGTC
 P D D F A T Y Y C H Q R S T Y P L T F G
 370 380 390 400
 AGGGGACCAAGGTGGAGGTCAAACGTAAGTACACTTTCTAGA
 Q G T K V E V K

FIGURE 18

HES12	AGCTTCTAATGGATGGAGCTGGATCTTCTCTTCCCTGTCAGGTACCCGGGGCGTG CACTCTCAGGTGGAGCTTGGAGCTGGAGCTGGAGCTGGTGAAGTCAAGAACCTGGCTCAGGCTC AAGGTC
HES13	CCAGTCACGGATTAATATAATCCATTCCAGACCCCTGTCAGGGCCTGCGCTTAC CGAGTCATCCTGTAAGCTACTAAGGTGTAAGGCTGACCCCTTCCAGGAGACCTTCAACGCT CGAGCCAGG
HES14	TATATTAAATCCGTCGACTGGTATACTGAATAATCAAGAAGTTCAAGGAAGGCAACA ATTACTGAGACCAATCCACCAATACAGCCTACATGGAACTGAGATCTGAG GACA
HES15	ATATCGCTCTAGAGCTTTAAGGACTCACCTAGGAGACTGTGACCAAGGGTTCCTTGGCC CACTACTCAAAGACCCCTCTTCCACACTAATAGACTGGCTCTCAGATCTC AGGCTGGT

FIGURE 19A

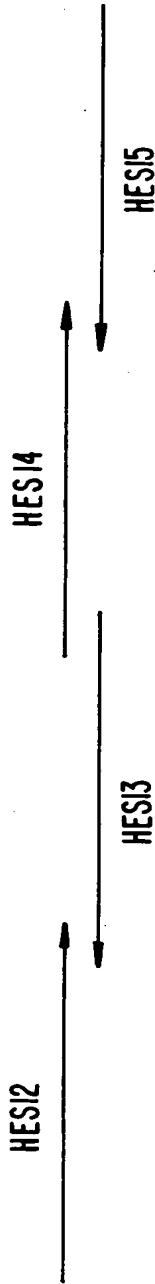


FIGURE 19B

JFD1	CAAATCTAGATGGAGACCGATACCCCTCTGCTATGGCTCTCCCTGCTATGGCTCCAGGA TCAAACGGAGATATTAGATGAGCTGGATGAGCTGGATCTACCTCTGGCTAGGGTGGAT
JFD2	ATAAATTAGAAGCTTGGGAGCTTGGCTGGCTTCTGCTGCTACCACTGCTAACTTAT ACCTGAGCTGGCAAGGAGCTTATGGTGAACCTATCCCACGGCTAGGAGAG
JFD3	GGTGGCAAGGCTCTAATTATAAGACATGGAAACCTGGCTCTGGAGTCCCTGCTCGCTTC AGTGGCACTGGATCTGGACGGAGTTCAACCTACAATCAAGCTGCTGGACCCAGATGAT TTC
JFD4	TATACTAGAAAAGTGTACTTACCTTACCTTGGCTGGCTGGCTGACCGAACGCTGAG TGGGTAAGTACTGGCTTGTGGCACTATAAGTGGCAATCATCTGGCTGAGAGCT GA

FIGURE 20A

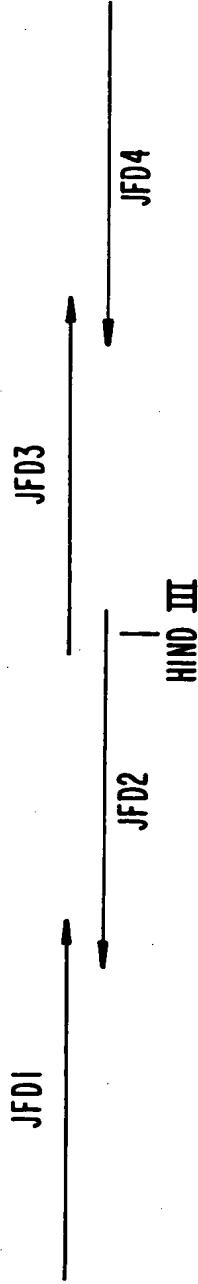


FIGURE 20B

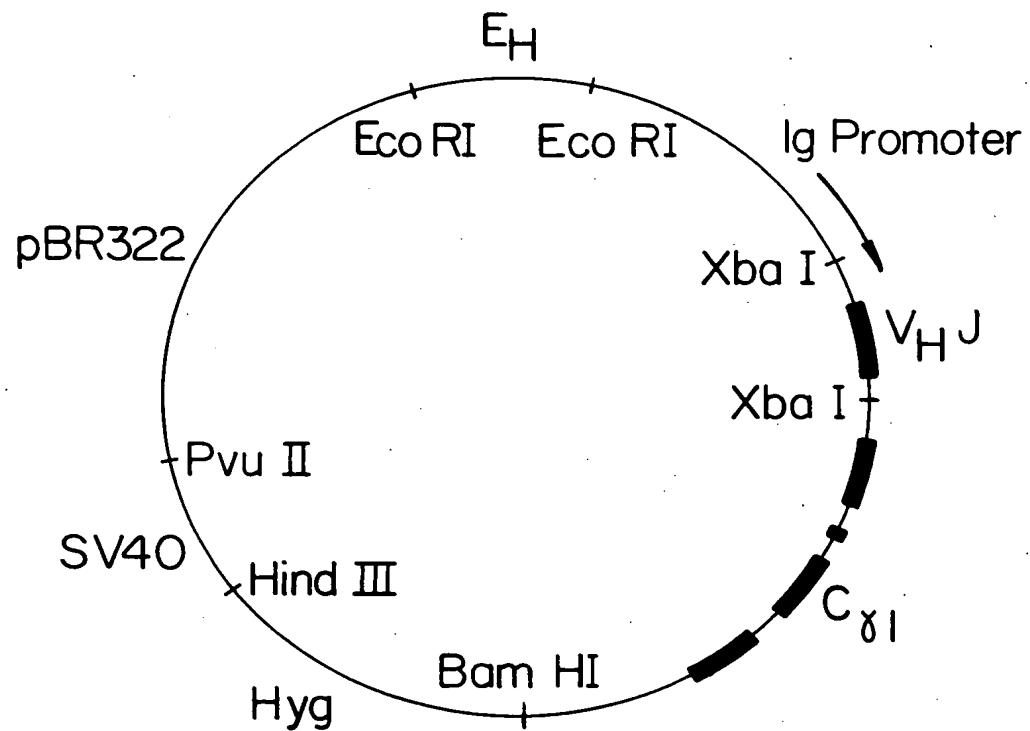


FIGURE 21

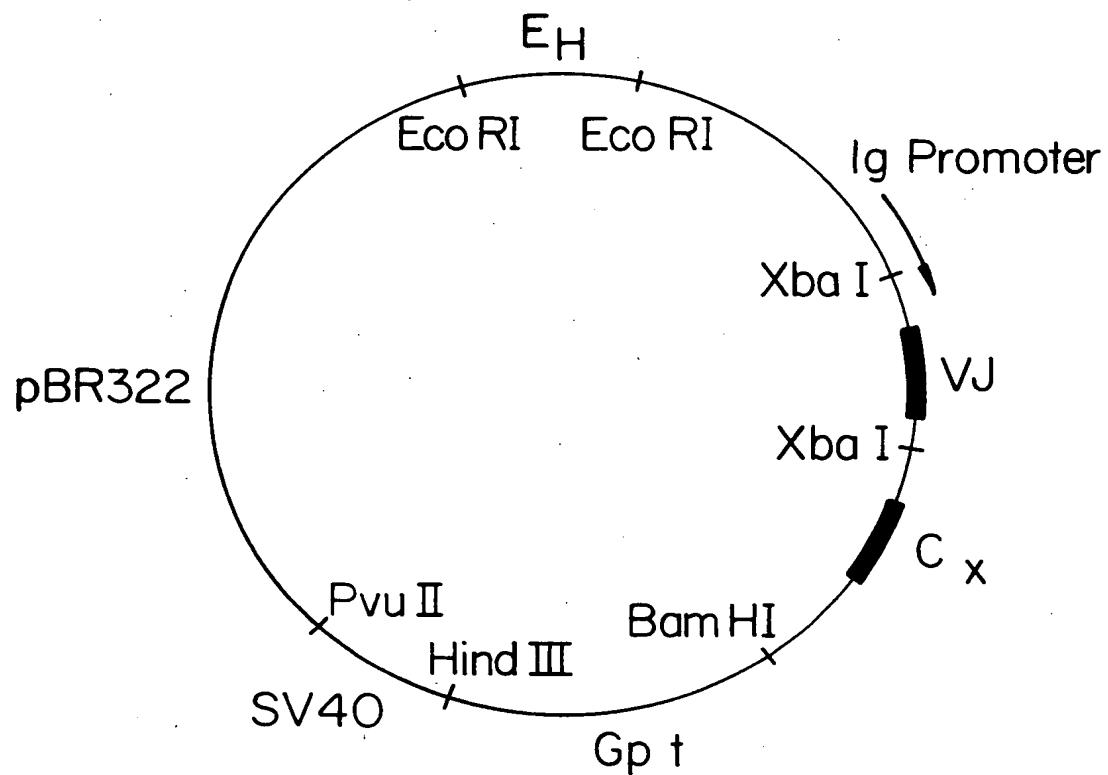


FIGURE 22

30 60
 ATGGATTTCAGAGTTTCAGCTCCTGCTAATCAGTCAGTCATACTGTCC
 M D F Q V Q I F S F L L I S A S V I L S
 90 120
 AGAGGACAAATTGTTCTCACCCAGTCTCCAGCAATCATGTCAGTCAGGGCGAAG
 R G Q I V L T Q S P A I M S A S P G E K
 150 180
 GTCACCATGACCTGCAGTGGCAGCTCAAGTGTAAAGTTCATGTAAGTGGTACCGAGCAGAGG
 V T M T C S G S S V S F M Y W Y Q Q R
 210 240
 CCAGGATCCTCCCCAGACTCCTGATTATGACACATCCAACCTGGCTCTGGAGTCCCT
 P G S S P R L L I Y D T S N L A S G V P
 270 300
 GTTCGCTTCAGTGGCAGTGGTCTGGGACCTCTTACTCTCACAATCAGCCGAATGGAG
 V R F S G S G T S Y S L T I S R M E
 330 360
 GCTGAAGATGCTGCCACTTATTACTGCCAGCAGTGGAGTACTTACCCGCTCACGTTGGT
 A E D A A T Y Y C Q Q W S T Y P L T F G

 GCTGGGACCAAGCTGGAGCTGAAA
 A G T K L E L K

FIGURE 23A

30 60
 ATGGCTGTCTGGGCTGCTCTGCTGGTGACATTCCAAGCTGTGTCCTATCCCAG
 M A V L G L L F C L V T F P S C V L S Q
 90 120
 GTGCAGCTGAAGCAGTCAGGACCTGGCCTAGTGCAGCCCTCACAGAGCCTGTCCATCACC
 V Q L K Q S G P G L V Q P S Q S L S I T
 150 180
 TGCACAGTCTGGTTCTCAGTAACAAGTTATGGTGACTGGATTGCCAGTCTCCA
 C T V S G F S V T S Y G V H W I R Q S P
 210 240
 GGAAAGGGTCTGGAGTGGCTGGAGTGATATGGAGTGGTGGAAAGCACAGACTATAATGCA
 G K G L E W L G V I W S G G S T D Y N A
 270 300
 GCTTCATATCCAGACTGACCATCAGCAAGGACAACCTCAAGAGCCAAGTTCTTAAA
 A F I S R L T I S K D N S K S Q V F F K
 330 360
 GTGAACAGTCTGCAACCTGCTGACACAGCCATATACTATTGTGCCAGAGCTGGGACTAT
 V N S L Q P A D T A I Y Y C A R A G D Y
 390
 AATTACGACGGTTTGCTTACTGGGGCCAAGGGACTCTGGTCACTGTCTGCG
 N Y D G F A Y W G Q G T L V T V S A

FIGURE 23B

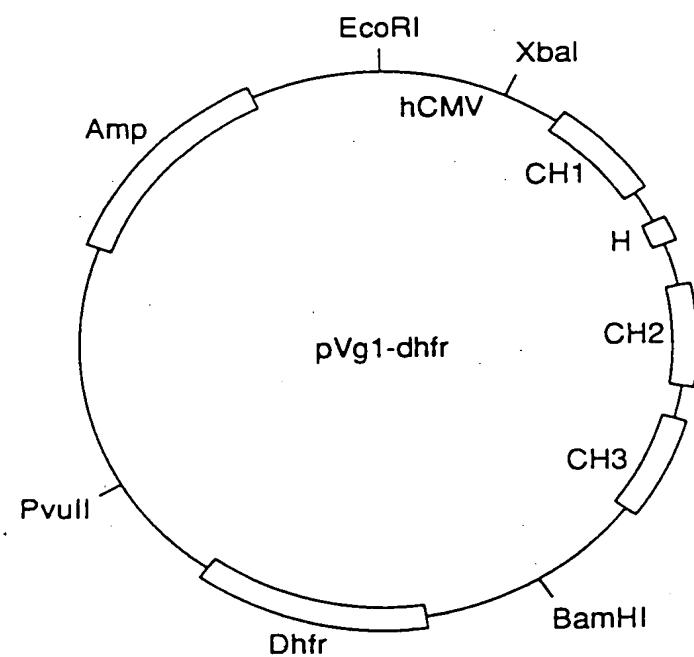


FIGURE 24A

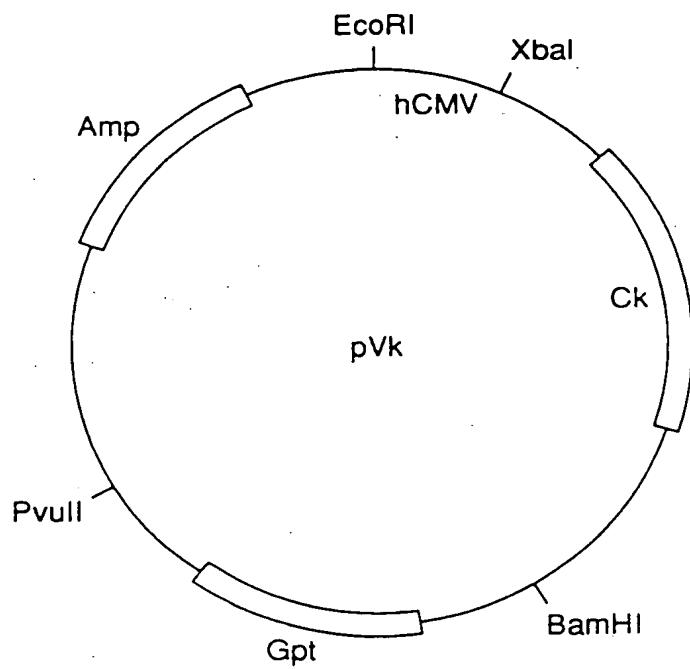


FIGURE 24B

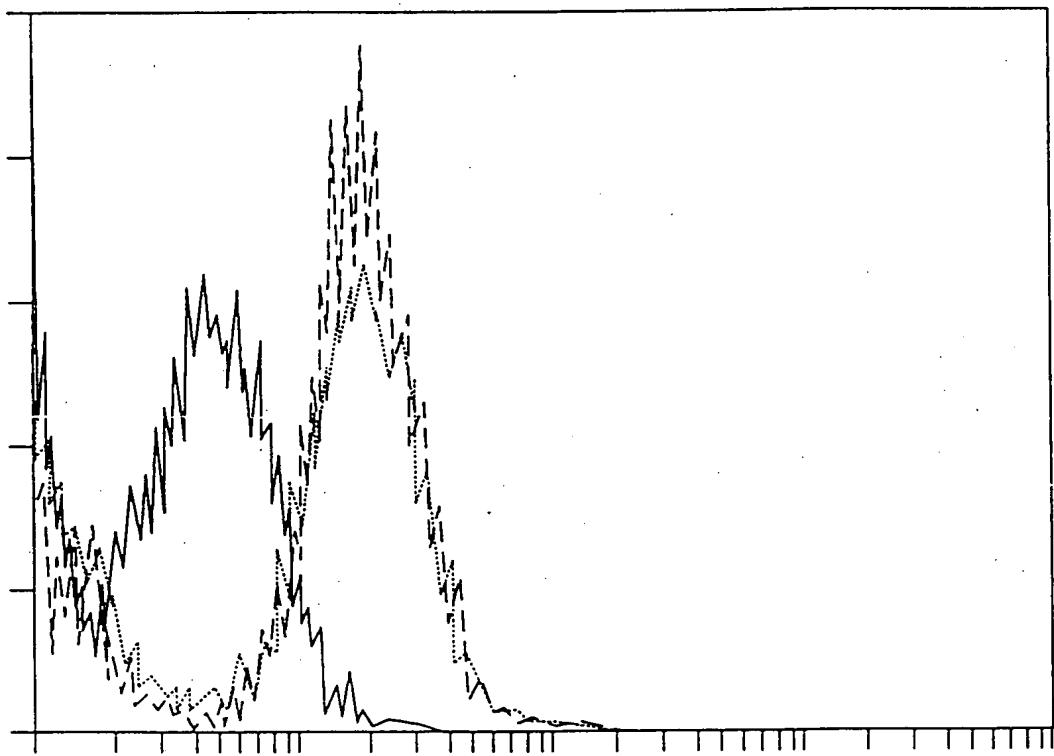


FIGURE 25

1	D	I	Q	M	T	Q	S	P	S	S	L	S	V	S	V	G	D	R	V	T
1	D	I	Q	M	T	Q	S	P	S	S	L	S	<u>A</u>	S	V	G	D	R	V	T
21	I	T	C	Q	A	S	Q	N	V	N	A	Y	L	N	W	Y	Q	Q	K	P
21	I	T	C	<u>S</u>	G	S	S	V		S	F	M	Y	W	Y	Q	Q	K	P	
41	G	L	A	P	K	L	L	I	Y	G	A	S	T	R	E	A	G	V	P	S
40	G	<u>K</u>	A	P	K	L	L	I	Y	<u>D</u>	T	S	N	L	A	S	G	V	P	S
61	R	F	S	G	S	G	S	G	T	D	F	T	F	T	I	S	S	L	Q	P
60	R	F	S	G	S	G	S	G	T	D	<u>Y</u>	T	F	T	I	S	S	L	Q	P
81	E	D	I	A	T	Y	Y	C	Q	Q	Y	N	N	W	P	P	T	F	G	Q
80	E	D	I	A	T	Y	Y	C	<u>Q</u>	<u>Q</u>	W	S	T	Y	P	L	T	F	G	Q
101	G	T	K	V	E	V	K													
100	G	T	K	V	E	V	K													

FIGURE 26A

1	A	V	Q	L	L	E	S	G	G	G	L	V	Q	P	G	G	S	L	R	L
1	<u>E</u>	V	Q	L	L	E	S	G	G	G	L	V	Q	P	G	G	S	L	R	L
21	S	C	A	A	S	G	F	T	F	S	A	S	A	M	S	W	V	R	Q	A
21	S	C	A	A	S	G	F	T	<u>V</u>	<u>T</u>	<u>S</u>	<u>Y</u>	G	V	H	W	V	R	Q	A
41	P	G	K	G	L	E	W	V	A	W	K	Y	E	N	G	N	D	K	H	Y
41	P	G	K	G	L	E	W	V	<u>G</u>		<u>V</u>	<u>I</u>	W	S	G	G	S	T	D	Y
61	A	D	S	V	N	G	R	F	T	I	S	R	N	D	S	K	N	T	L	Y
60	N	A	A	F	I	S	R	F	T	I	S	R	<u>D</u>	<u>N</u>	S	K	N	T	L	Y
81	L	Q	M	N	G	L	Q	A	Z	V	S	A	I	Y	Y	C	A	R	D	A
80	L	Q	M	N	<u>S</u>	L	Q	A	E	<u>D</u>	<u>T</u>	A	I	Y	Y	C	A	R	<u>A</u>	
101	G	P	Y	V	S	P	T	F	F	A	H	W	G	Q	G	T	L	V	T	V
99	G	D	Y	N	Y	D	G	F	A	Y	W	G	Q	G	T	L	V	T	V	
121	S	S																		
118	S	S																		

FIGURE 26B

vc13

10 20 30 40 50 60
TTCTGCTGGT ACCAGTACAT GAAACTTACA CTTGAGCTGC CACTGCAGGT GATGGTGACG
70 80 90 100
CGGTCACCCA CTGAGGCACT GAGGCTAGAT GGAGACTGGG TCATTTG

vc14

10 20 30 40 50 60
CATGTACTGG TACCAGCAGA AGCCAGGAAA AGCTCCGAAA CTTCTGATTT ATGACACATC
70 80 90 100 110 120
CAACCTGGCT TCTGGAGTCC CTTCCCGCTT CAGTGGCAGT GGGTCTGGGA CCGATTACAC
130
CTTTACAATC TCTTCA

vc15

10 20 30 40 50 60
TGTGTCTAGA AAAGTGTACT TACGTTTAC CTCGACCTTG GTCCCTTGAC CGAACGTGAG
70 80 90 100 110 120
CGGGTAAGTA CTCCACTGCT GGCAGTAATA AGTGGCTATA TCTTCCGGCT GAAGTGAAGA
130
GATTGTAAAG GTGTAAT

vc16

10 20 30 40 50 60
CACATCTAGA CCACCATGGA TTTTCAAGTG CAGATCTTCA GCTTCCTGCT AATCAGTGCC
70 80 90 100
TCAGTCATAC TGTCCAGAGG AGATATTCAA ATGACCCAGT CTCCATCT

FIGURE 27A

vc11

10 20 30 40 50 60
TAGTCTGTCG ACCCACCACT CCATATCACT CCCACCCACT CGAGTCCCTT TCCAGGAGCC
70 80 90 100 110 120
TGGCGGACCC AGTGTACACC ATAACTTGTT ACGGTGAAAC CACTGGCGGC ACAAGACAGT
130
CTCAGAGATC CTCCTGGC

vc12

10 20 30 40 50 60
TGGTGGGTCG ACAGACTATA ATGCAGCTTT CATATCCAGA TTTACCATCA GCAGAGACAA
70 80 90 100 110 120
CAGCAAGAAC ACACTGTATC TCCAAATGAA TAGCCTGCAA GCCGAGGACA CAGCCATATA

TTATTG

wps54

10 20 30 40 50 60
ACACTCTAGA CCACCATGGC TGTCTGGGG CTGCTCTTCT GCCTGGTGAC ATTCCAAGC
70 80 90 100 110 120
TGTGTCCTAT CCGCTGTCCA GCTGCTAGAG AGTGGTGGCG GTCTGGTGCA GCCAGGAGGA
130
TCTCTGAGAC

wps57

10 20 30 40 50 60
ACACTCTAGA AGTTAGGACT CACCTGAAGA GACAGTGACC AGAGTCCCTT GGCCCCAGTA
70 80 90 100 110
AGCAAAACCG TCGTAATTAT AGTCCCCAGC TCTGGCACAA TAATATATGG CTGTGTCC

FIGURE 27B

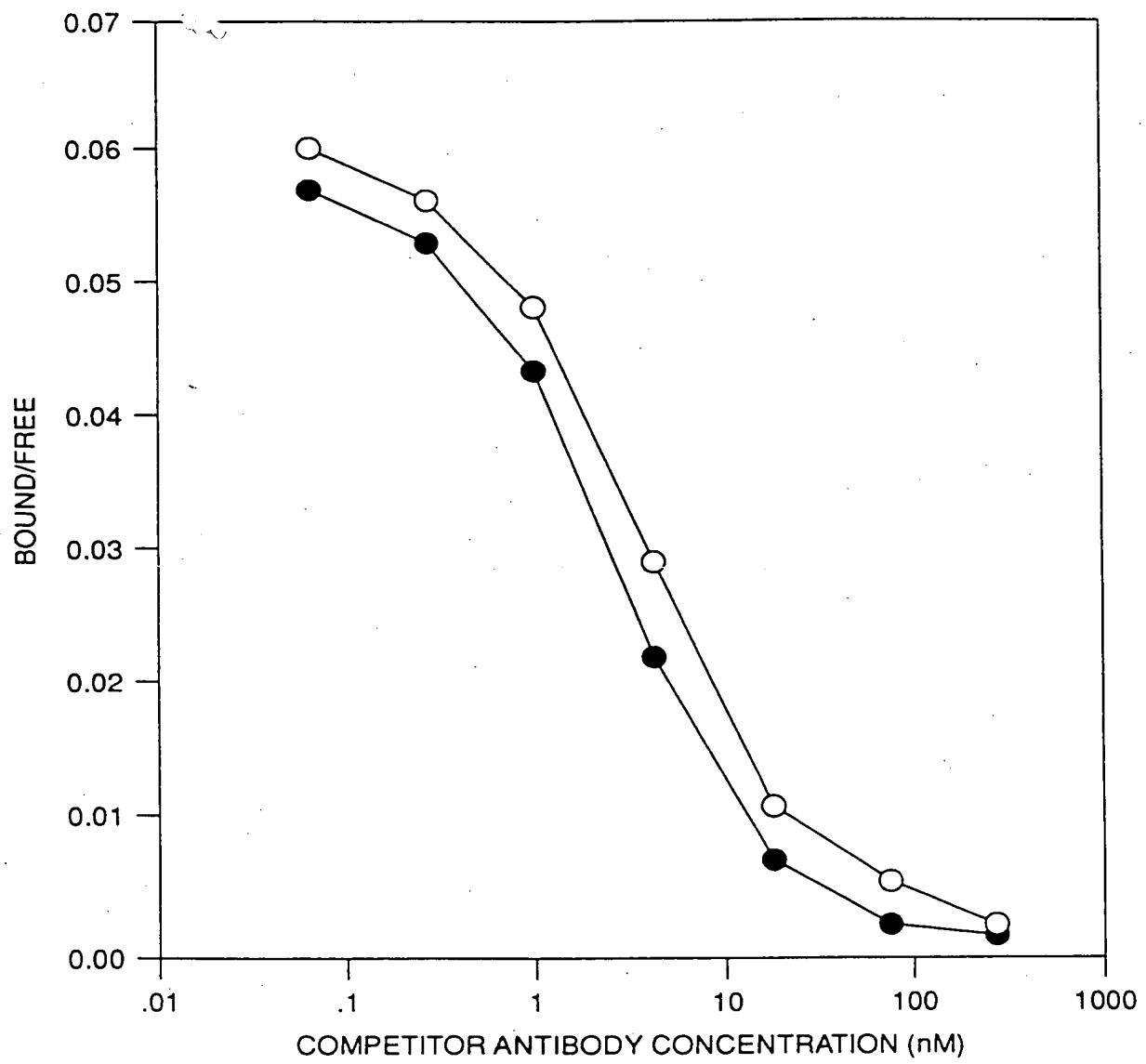


FIGURE 28

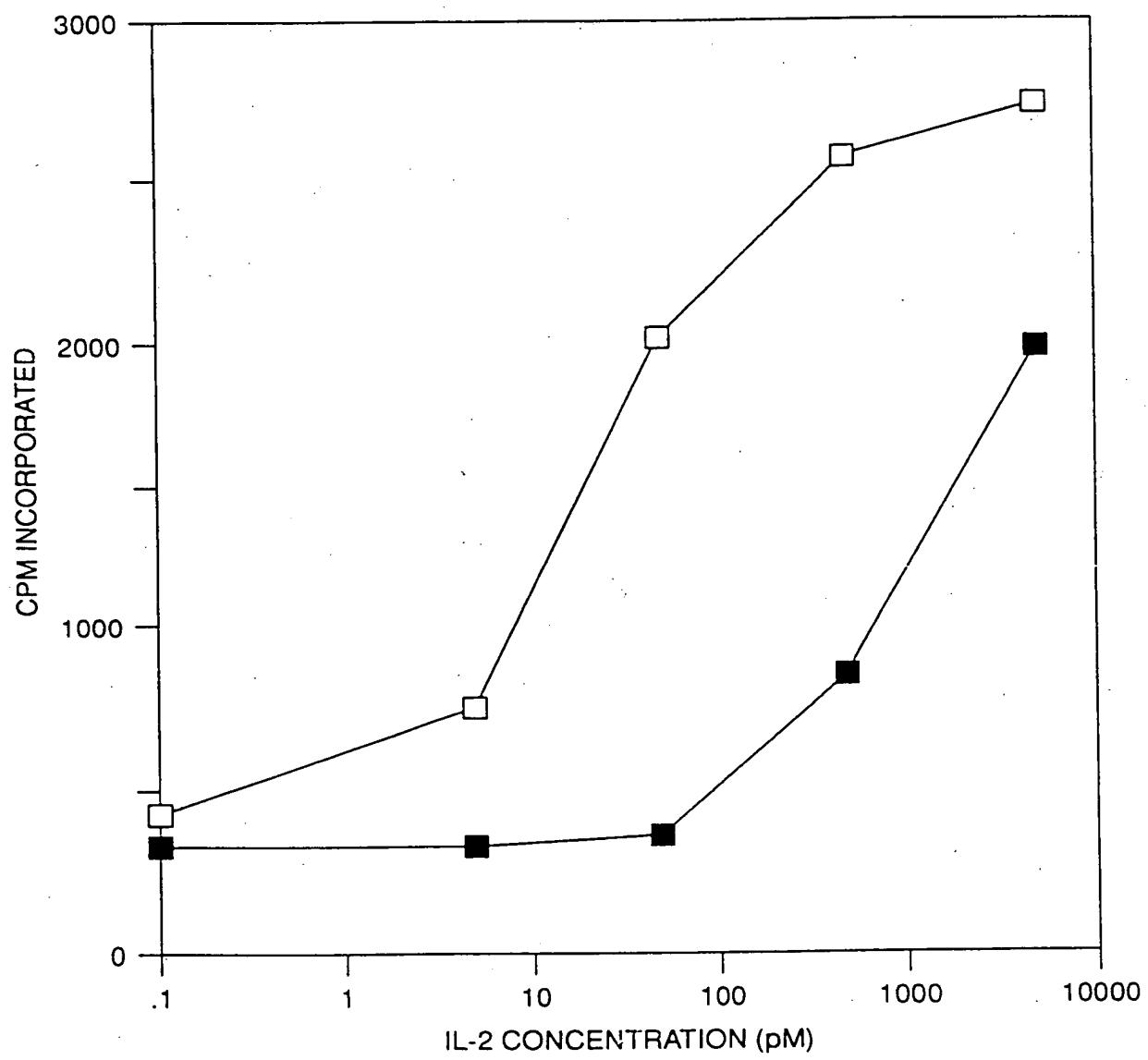


FIGURE 29

	1	5	10	15	20
1	E M I L V E S G G G L V K P G A S L K L				
1	E V Q L L E S G G G G L V Q P G G S L R L				
	25	30	35		40
21	S C A A S G F T F S N Y G L S W V R Q T				
21	S C A A S G F T F S N Y G L S W V R Q A				
	45	50	52 a	55	
41	S D R R L E W V A S I S R G G G R I Y S				
41	P G K G L E W V A S I S R G G G R I Y S				
	60	65	70	75	
60	P D N L K G R F T I S R E D A K N T L Y				
60	P D N L K G R F T I S R N D S K N T L Y				
	80	82 a b c	85	90	95
80	L Q M S S L K S E D T A L Y Y C L R E G				
80	L Q M N S L Q A E D T A L Y Y C L R E G				
	100 a b c d k		105		110
97	I Y Y A D Y G F F D V W G T G T T V I V				
97	I Y Y A D Y G F F D V W G Q G T L V T V				
	113				
112	S S				
112	S S				

FIGURE 30A

	1	5	10	15	20
1	D I V L T Q S P A S L A V S L G Q R A T				
1	E I V M T Q S P <u>A</u> T L S V S P G E R A T				
	25	27 a b c d	30		35
21	I S C R A S Q S V S T S T Y N Y M H W Y				
21	L S C R A S Q S V S T S T Y N Y M H W Y				
	40	45	50	55	
37	Q Q K P G Q P P K L L I K Y A S N L E S				
37	Q Q K P <u>G</u> Q S P R L L I <u>K</u> Y A S N L E S				
	60	65	70	75	
57	G V P A R F S G S G F G T D F T L N I H				
57	G I P A R F S G S G S G T E F T L T I S				
	80	85	90	95	
77	P V E E E D T V T Y Y C Q H S W E I P Y				
77	<u>R</u> L <u>E</u> S E D F A V Y Y C Q H S W E I P Y				
	100	105	107		
97	T F G G G T K L E I K				
97	T F G Q G T R V E I K				

FIGURE 30B

	1	5	10	15	20
1	Q V Q L Q Q S D A E L V K P G A S V K I				
1	Q V Q L V Q S G A E V K K P G S S V K V				
	25	30	35		40
21	S C K V S G Y T F T D H T I H W M K Q R				
21	S C K A S G Y T F T D H T I H W M R Q A				
	45	50	52 a	55	
41	P E Q G L E W F G Y I Y P R D G H T R Y				
41	P G Q G L E W F G Y I Y P R D G H T R Y				
	60	65	70	75	
60	S E K F K G K A T L T A D K S A S T A Y				
60	A E K F K G K A T I T A D E S T N T A Y				
	80	82 a b c	85	90	95
80	M H L N S L T S E D S A V Y F C A R G R				
80	M E L S S L R S E D T A V Y F C A R G R				
	100 a b c d		105		110
97	D S R E R N G F A Y W G Q G T L V T V S				
97	D S R E R N G F A Y W G Q G T L V T V S				
	113				
113	A				
113	S				

FIGURE 30C

	1	5	10	15	20
1	D I V M T Q S H K F M S T S V G D R V S				
1	D I Q M T Q S P S T L S A S V G D R V T				
	25	30	35		40
21	I T C K A S Q D V G S A V V W H Q Q K S				
21	I T C K A S Q D V G S A V V W H Q Q K P				
	45	50	55		60
41	G Q S P K L L I Y W A S T R H T G V P D				
41	G K A P K L L I Y W A S T R H T G V P S				
	65	70	75		80
61	R F T G S G S G T D F T L T I T N V Q S				
61	R F T G S G S G T E F T L T I S S L Q P				
	85	90	95		100
81	E D L A D Y F C Q Q Y S I F P L T F G A				
81	D D F A T Y F C Q Q Y S I F P L T F G Q				
	105 107				
101	G T R L E L K				
101	G T K V E V K				

FIGURE 30D

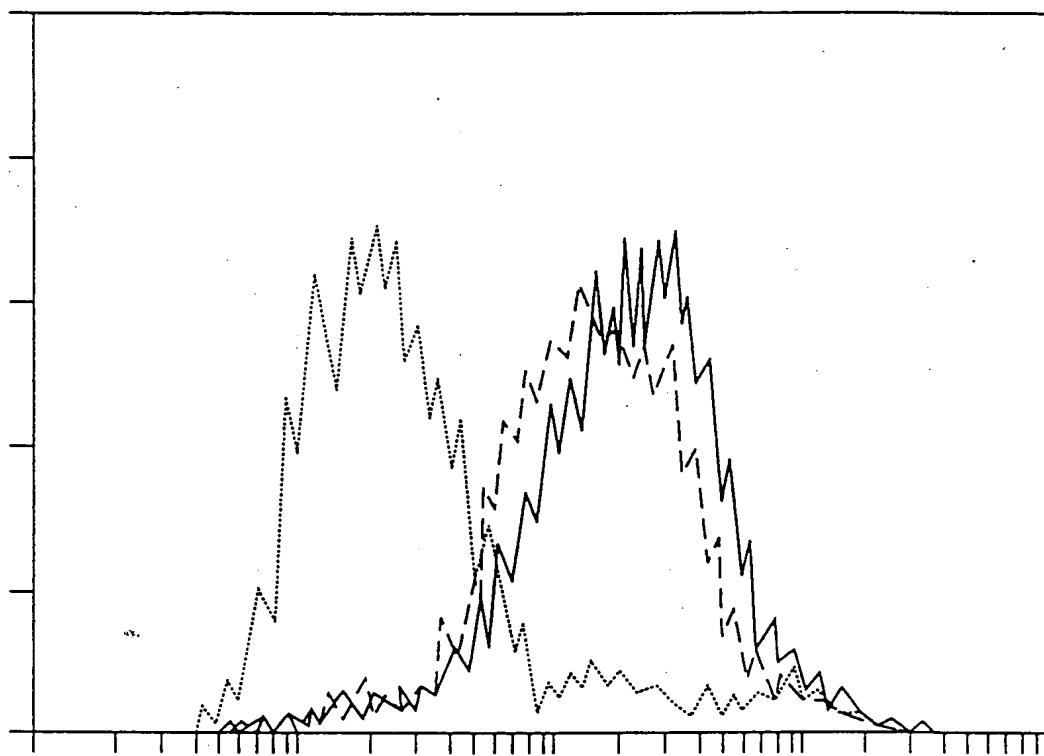


FIGURE 31A

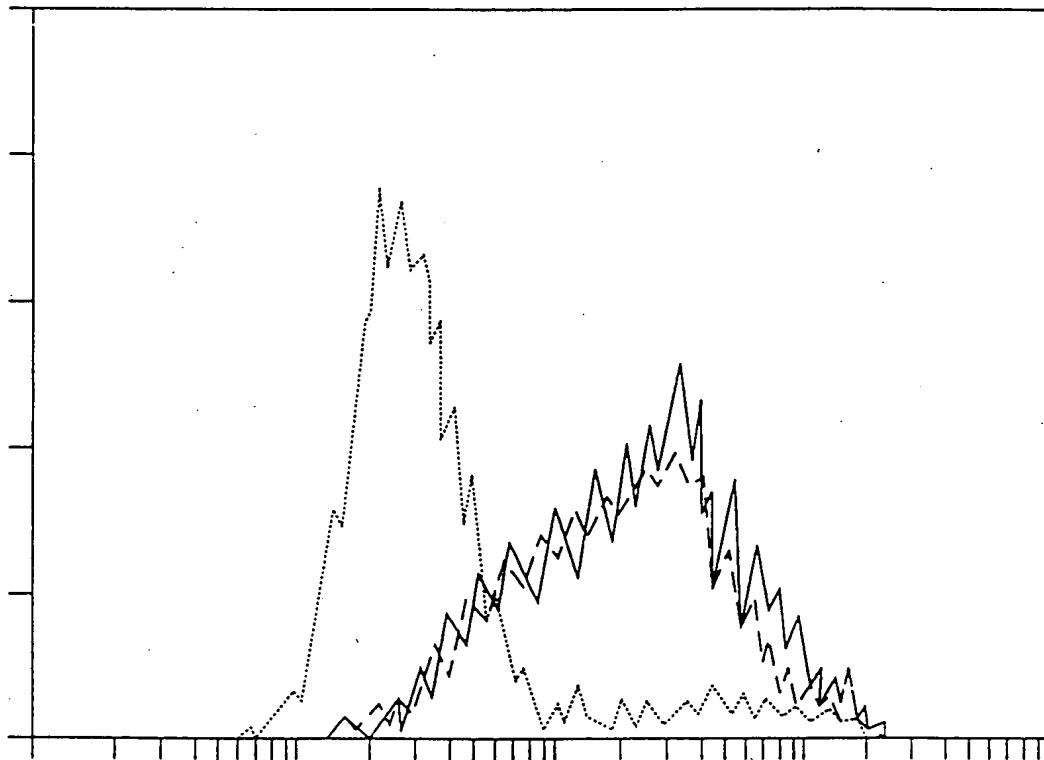


FIGURE 31B

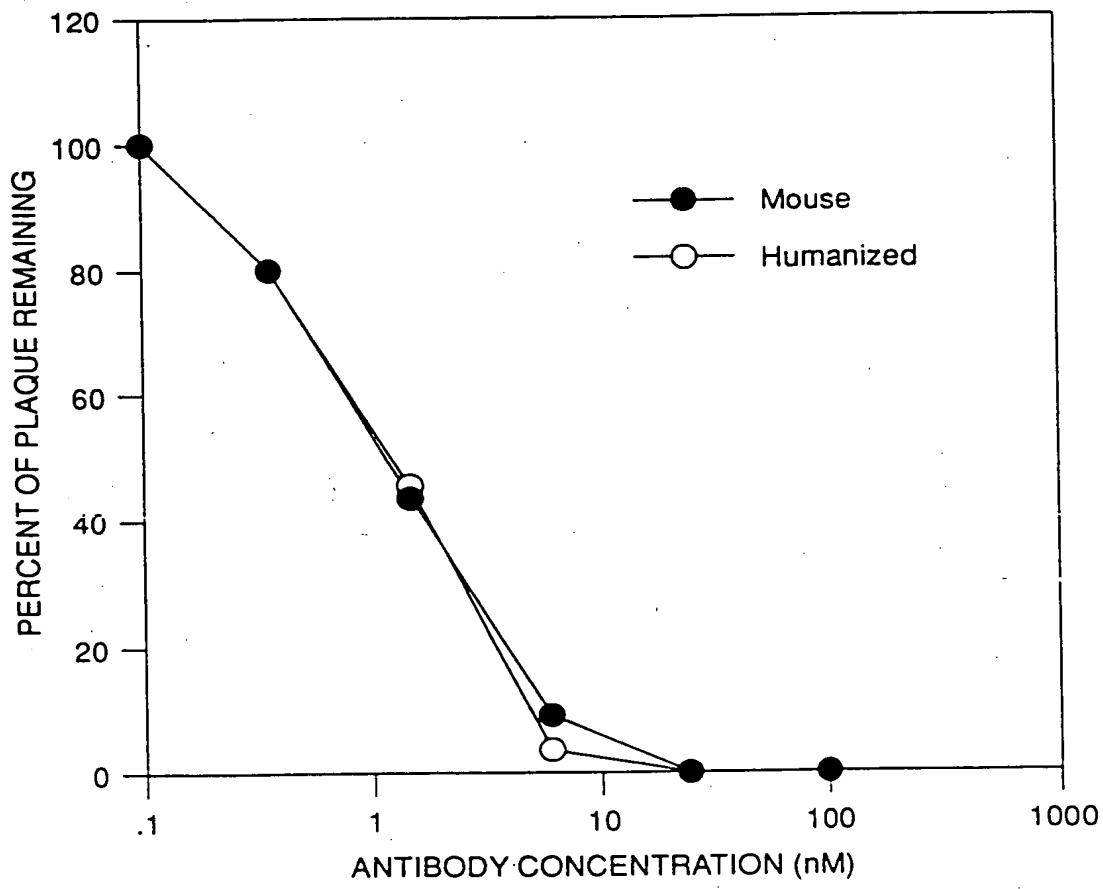


FIGURE 32A

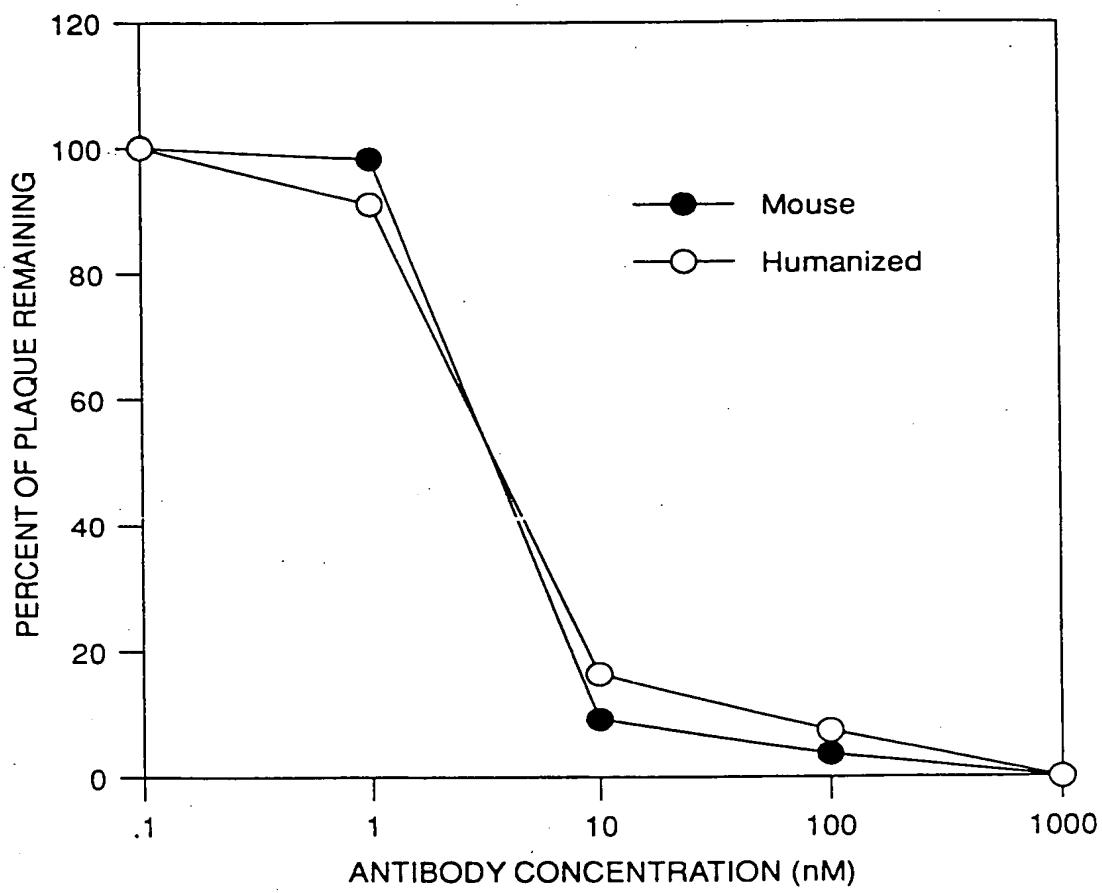


FIGURE 32B

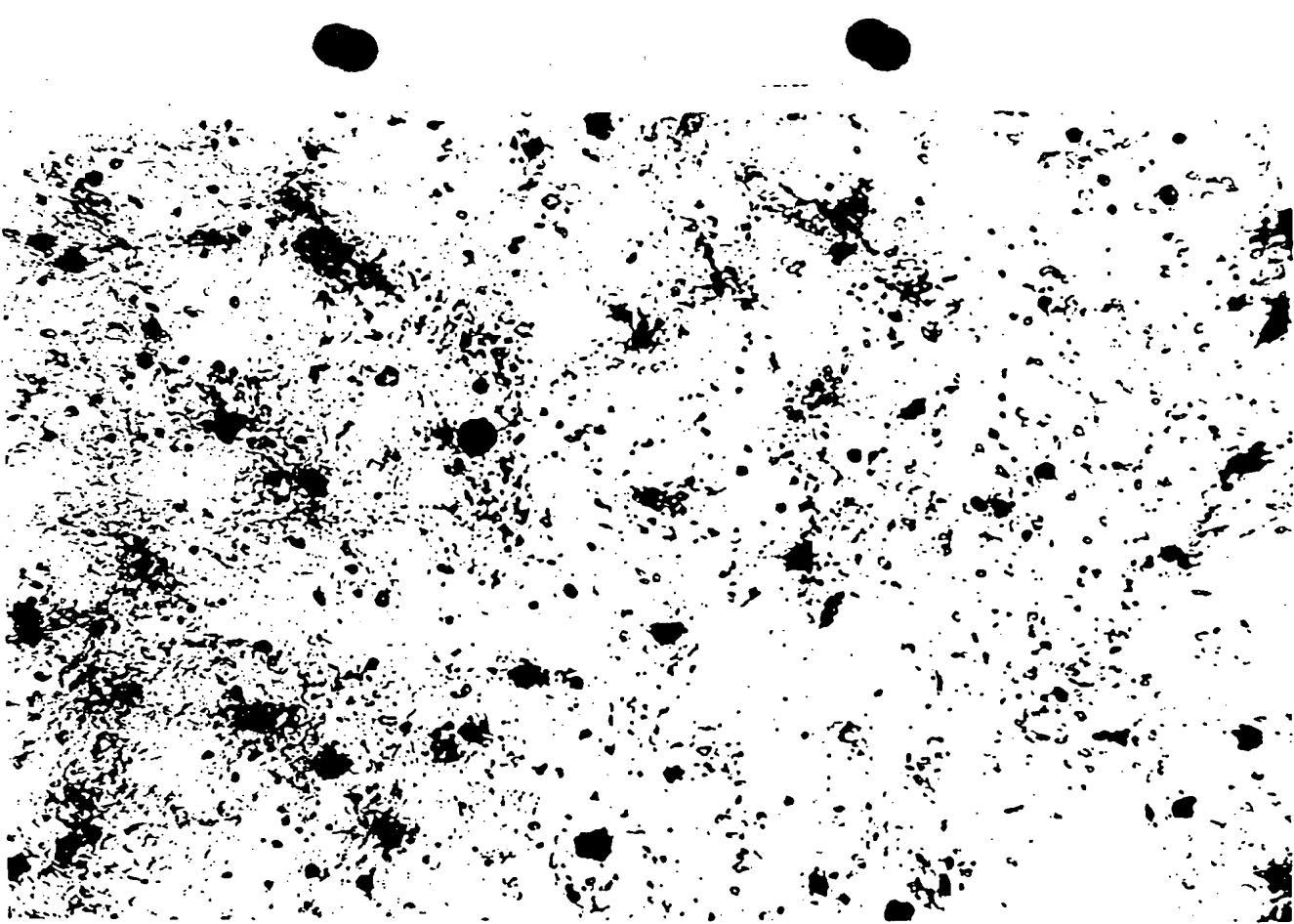


FIGURE 33A



FIGURE 33B

30 60
 ATGGAGAAAGACACACTCCTGCTATGGGCTCTGCTTCTGGGTTCCAGGTTCCACAGGT
 M E K D T L L L W V L L L W V P G S T G
 90 120
 GACATTGTGCTGACCCAATCTCCAGCTTCTTGCTGTGTCTCTAGGGCAGAGGGCCACC
 D I V L T Q S P A S L A V S L G Q R A T
 150 180
 ATCTCCTGCAGAGCCAGCGAAAGTGTGATAATTATGGCATTAGTTTATGAACGTGGTC
 I S C R A S E S V D N Y G I S F M N W F
 210 240
 CAACAGAAACCAGGACAGCCACCCAAACTCCTCATCTATGCTGCATCCAACCAAGGATCC
 Q Q K P G Q P P K L L I Y A A S N Q G S
 270 300
 GGGTCCCTGCCAGGTTAGTGGCAGTGGTCTGGGACAGACTTCAGCCTAACATCCAT
 G V P A R F S G S G S G T D F S L N I H
 330 360
 CCTATGGAGGAGGATGATACTGCAATGTATTCCTGTCAGCAAAGTAAGGAGGTTCCGTGG
 P M E E D D T A M Y F C Q Q S K E V P W
 390
 ACGTTCGGTGGAGGCACCAAGCTGGAAATCAA
T F G G G T K L E I K

FIGURE 34A

. 30 60
 ATGGGATGGAGCTGGATCTTCTCTCCTGTCAGGAAC TG CAGGCGTCCACTCTGAG
 M G W S W I F L F L L S G T A G V H S E
 90 120
 GTCCAGCTTCAGCAGTCAGGACCTGAGCTGGTGAACCTGGGCCCTCAGTGAAGATATCC
 V Q L Q Q S G P E L V K P G A S V K I S
 150 180
 TGCAAGGCTTCTGGATACACATTCACTGACTACAACATGCACTGGGTGAAGCAGAGCCAT
 C K A S G Y T F T D Y N M H W V K Q S H
 210 240
 GGAAAGAGCCTTGAGTGGATTGGATATTTATCCTTACAATGGTGGTACTGGCTACAAAC
 G K S L E W I G Y I Y P Y N G G T G Y N
 270 300
 CAGAAAGTTCAAGAGCAAGGCCACATTGACTGTAGACAATTCCCTCAGCACAGCCTACATG
Q K F K S K A T L T V D N S S S T A Y M
 330 360
 GACGTCCGCAGCCTGACATCTGAGGACTCTGCAGTCTATTACTGTGCAAGAGGGCGCCCC
 D V R S L T S E D S A V Y Y C A R G R P
 390
 GCTATGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCA
A M D Y W G Q G T S V T V S S

FIGURE 34B

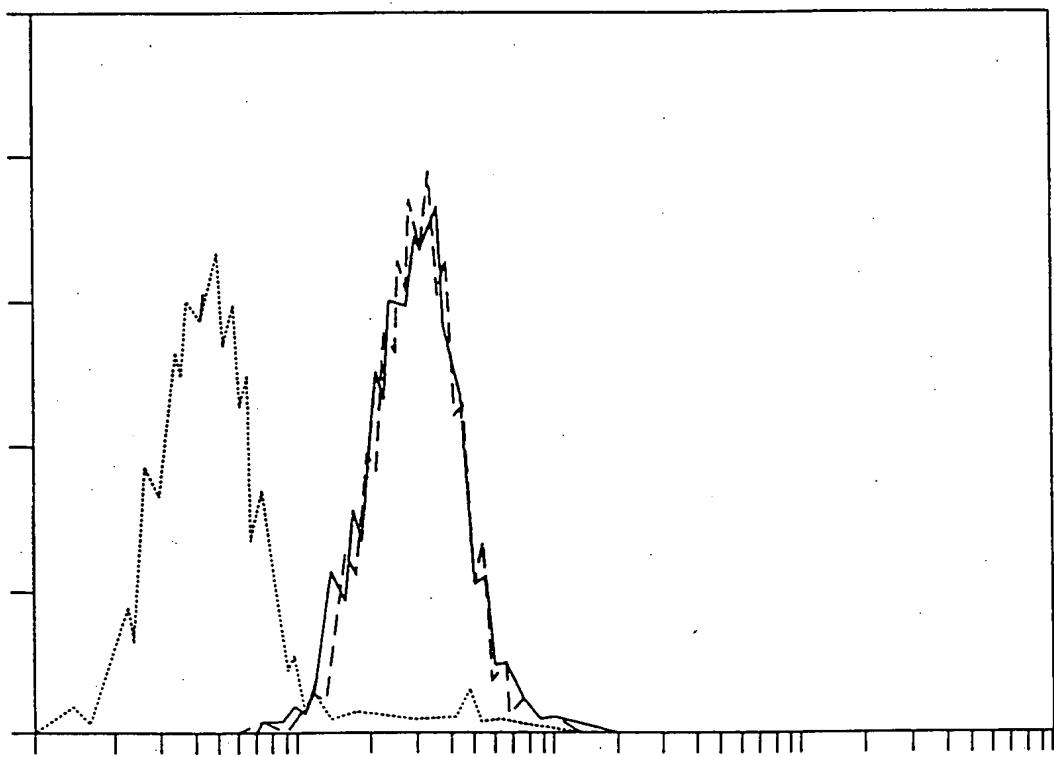


FIGURE 35

1	D	I	Q	M	T	Q	S	P	S	T	L	S	A	S	V	G	D	R	V	T
1	D	I	Q	M	T	Q	S	P	<u>S</u>	S	L	S	A	S	V	G	D	R	V	T
21	I	T	C	R	A	S	Q	S	I	N					T	W	L	A	W	Y
21	I	T	C	<u>R</u>	A	S	E	S	V	D	N	Y	G	I	S	F	M	N	W	<u>F</u>
37	Q	Q	K	P	G	G	A	P	K	L	L	M	Y	K	A	S	S	L	E	S
41	Q	Q	K	P	G	G	A	P	K	L	L	<u>I</u>	Y	<u>A</u>	<u>A</u>	S	N	Q	G	S
57	G	V	P	S	R	F	I	G	S	G	S	G	T	E	F	T	L	T	I	S
61	G	V	P	S	R	F	<u>S</u>	G	S	G	S	G	T	<u>D</u>	F	T	L	T	I	S
77	S	L	Q	P	D	D	F	A	T	Y	Y	C	Q	Q	Y	N	S	D	S	K
81	S	L	Q	P	D	D	F	A	T	Y	Y	C								
97	M	F	G	Q	G	T	K	V	E	V	K									
101	<u>T</u>	F	G	Q	G	T	K	V	E	<u>I</u>	K									

FIGURE 36A

1	Q	V	Q	L	V	Q	S	G	A	E	V	K	K	P	G	S	S	V	K	V
1	Q	V	Q	L	V	Q	S	G	A	E	V	K	K	P	G	S	S	V	K	V
21	S	C	K	A	S	G	G	T	F	S	R	S	A	I	I	W	V	R	Q	A
21	S	C	K	A	S	G	T	F	D	Y	N	M	H	W	V	R	Q	A		
41	P	G	Q	G	L	E	W	M	G	G	I	V	P	M	F	G	P	P	N	Y
41	P	G	Q	G	L	E	W	G	I	Y	P	Y	N	G	G	T	G	Y		
61	A	Q	K	F	Q	G	R	V	T	I	T	A	D	E	S	T	N	T	A	Y
61	<u>N</u>	<u>Q</u>	<u>K</u>	<u>F</u>	<u>K</u>	<u>S</u>	T	I	T	A	D	E	S	T	N	T	A	Y		
81	M	E	L	S	S	L	R	S	E	D	T	A	F	Y	F	C	A	G	G	Y
81	M	E	L	S	S	L	R	S	E	D	T	A	C	A						
101	G	I	Y	S	P	E	E	Y	N	G	G	L	V	T	V	S	S			
100	<u>R</u>	<u>P</u>	<u>A</u>	<u>M</u>	<u>D</u>	<u>Y</u>	G	L	V	T	V	S	S							

FIGURE 36B

ma1

10 20 30 40 50 60
TATATCTAGA CCACCATGGG ATGGAGCTGG ATCTTTCTCT TCCTCCTGTC AGGAACTGCT
70 80 90 100 110 120
GGCGTCCACT CTCAGGTTCA GCTGGTGCAG TCTGGAGCTG AGGTGAAGAA GCCTGGGAGC
130
TCAGTGAAGG TT

ma2

10 20 30 40 50 60
AGCCGGTACC ACCATTGTA GGATAAAATAT ATCCAATCCA TTCCAGGCCT TGGCCAGGAG
70 80 90 100 110 120
CCTGCCTCAC CCAGTGCATG TTGTAGTCAG TGAAGGTGTA GCCAGAAGCT TTGCAGGAAA
130
CCTTCACTGA GCT

ma3

10 20 30 40 50 60
TGGTGGTACC GGCTACAACC AGAAGTTCAA GAGCAAGGCC ACAATTACAG CAGACGAGAG
70 80 90 100 110
TACTAACACA GCCTACATGG AACTCTCCAG CCTGAGGTCT GAGGACACTG CA

ma4

10 20 30 40 50 60
TATATCTAGA GGCCATTCTT ACCTGAAGAG ACAGTGACCA GAGTCCCTTG GCCCCAGTAG
70 80 90 100 110
TCCATAGCGG GGCGCCCTCT TGCGCAGTAA TAGACTGCAG TGTCCCTCAGA C

FIGURE 37A

ma5

10	20	30	40	50	60
TATATCTAGA CCACCATGGA GAAAGACACA CTCCTGCTAT GGGTCCTGCT TCTCTGGGTT					
70	80	90	100	110	120
CCAGGTTCCA CAGGTGACAT TCAGATGACC CAGTCTCCGA GCTCTCTGTC CGCATCAGTA					

GG

ma6

10	20	30	40	50	60
TCAGAAGCTT AGGAGCCTTC CCGGGTTTCT GTTGGAACCA GTTCATAAAG CTAATGCCAT					
70	80	90	100	110	120
AATTGTCGAC ACTTTCGCTG GCTCTGCATG TGATGGTGAC CCTGTCTCCT ACTGATGCGG					

AC

ma7

10	20	30	40	50	60
TCCTAAGCTT CTGATTTACG CTGCATCCAA CCAAGGCTCC GGGGTACCCCT CTCGCTTCTC					
70	80	90	100	110	
AGGCAGTGGAA TCTGGGACAG ACTTCACTCT CACCATTCA TCTCTGCAGC CTGATGACT					

ma8

10	20	30	40	50	60
TATATCTAGA CTTTGGATTC TACTTACGTT TGATCTCCAC CTTGGTCCCT TGACCGAACG					
70	80	90	100	110	
TCCACGGAAC CTCCTTACTT TGCTGACAGT AATAGGTTGC GAAGTCATCA GGCTGCAG					

FIGURE 37B

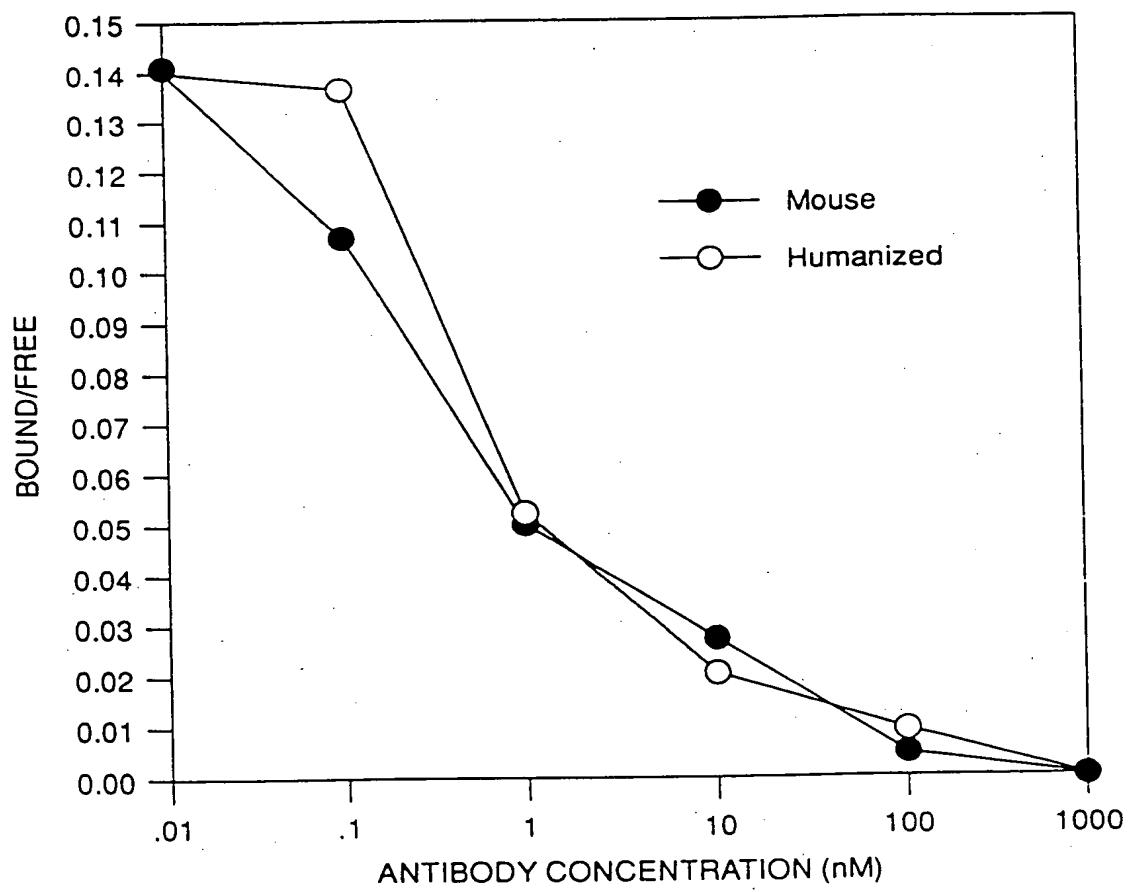


FIGURE 38

FIGURE 39A

30 60

ATGGGATGGAGCTGGATCTTCTCTCCTGTCAGGAAC TG CAGGTGTCCACTCTGAG
 M G W S W I F L F L L S G T A G V H S E

90 120

GTCCAGCTGCAACAGTCTGGACCTGAGCTGGTGAAGCCTGGAGCTTCAATGAAGATATCC
 V Q L Q Q S G P E L V K P G A S M K I S

150 180

TGCAAGGCTTCTGTTACTCATTCACTGGCTACACCATGAAC TG GGTGAAGCAGAGCCAT
 C K A S V Y S F T G Y T M N W V K Q S H

210 240

GGACAGAACCTTGAGTGGATTGGACTTATTAATCCTTACAATGGTGGTACTAGCTACAAC
 G Q N L E W I G L I N P Y N G G T S Y N

270 300

CAGAAGTTCAAGGGGAAGGCCACATTAACTGTAGACAAGTCATCCAACACAGCCTACATG
Q K F K G K A T L T V D K S S N T A Y M

330 360

GAGCTCCTCAGTCTGACATCTGCGGACTCTGCAGTCTATTACTGTACAAGACGGGGGTTT
 E L L S L T S A D S A V Y Y C I R R G F

390

CGAGACTATTCTATGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCA
 R D Y S M D Y W G Q G T S V T V S S

FIGURE 39B

1	E	I	V	L	T	Q	S	P	G	T	L	S	L	S	P	G	E	R	A	T
1	E	I	V	L	T	Q	S	P	G	T	L	S	L	S	P	G	E	R	A	T
21	L	S	C	R	A	S	Q	S	V	S	S	G	Y	L	G	W	Y	Q	Q	K
21	L	S	C	<u>R</u>	<u>A</u>	<u>S</u>	<u>Q</u>	<u>S</u>	<u>I</u>	<u>S</u>	<u>N</u>	<u>N</u>	<u>L</u>	<u>H</u>	<u>W</u>	<u>Y</u>	<u>Q</u>	<u>Q</u>	<u>K</u>	
41	P	G	Q	A	P	R	L	L	I	Y	G	A	S	S	R	A	T	G	I	P
40	P	G	Q	A	P	R	L	L	I	<u>K</u>	<u>Y</u>	<u>A</u>	<u>S</u>	<u>Q</u>	<u>S</u>	<u>I</u>	<u>S</u>	G	I	P
61	D	R	F	S	G	S	G	S	G	T	D	F	T	L	T	I	S	R	L	E
60	D	R	F	S	G	S	G	S	G	T	D	F	T	L	T	I	S	R	L	E
81	P	E	D	F	A	V	Y	Y	C	Q	Q	Y	G	S	L	G	R	T	F	G
80	P	E	D	F	A	V	Y	Y	C	Q	<u>Q</u>	<u>S</u>	<u>N</u>	<u>S</u>	<u>W</u>	<u>P</u>	<u>H</u>	<u>T</u>	<u>F</u>	<u>G</u>
101	Q	G	T	K	V	E	I	K												
100	Q	G	T	K	V	E	I	K												

FIGURE 40A

1	Q	V	Q	L	M	Q	S	G	A	E	V	K	K	P	G	S	S	V	R	V	
1	Q	V	Q	L	<u>V</u>	Q	S	G	A	E	V	K	K	P	G	S	S	V	R	V	
21	S	C	K	T	S	G	G	T	F	V	D	Y	K	G	L	W	V	R	Q	A	
21	S	C	K	<u>A</u>	S	<u>G</u>	<u>Y</u>	<u>S</u>	<u>F</u>	<u>T</u>	<u>G</u>	<u>Y</u>	<u>T</u>	<u>M</u>	<u>N</u>	<u>W</u>	<u>V</u>	<u>R</u>	<u>Q</u>	<u>A</u>	
41	P	G	K	G	L	E	W	V	G	Q	I	P	L	R	F	N	G	E	V	K	
41	P	G	K	G	L	E	W	V	G	<u>L</u>	<u>I</u>	<u>N</u>	<u>P</u>	<u>Y</u>	<u>N</u>	<u>G</u>	<u>G</u>	<u>T</u>	<u>S</u>	<u>Y</u>	
61	N	P	G	S	V	V	R	V	S	V	S	L	K	P	S	F	N	Q	A	H	
61	N	Q	K	F	K	G	R	V	<u>T</u>	V	S	L	K	P	S	F	N	Q	A	<u>Y</u>	
81	M	E	L	S	S	L	F	S	E	D	T	A	V	Y	Y	C	A	R	E	Y	
81	M	E	L	S	S	L	F	S	E	D	T	A	V	Y	Y	C	<u>T</u>	<u>R</u>	<u>R</u>		
101	G	F	D	T	S	D	Y	Y	Y	Y	W	G	Q	G	T	L	V	T	V		
100	G	F			R	D	Y	S	M	D	Y	W	G	Q	G	T	L	V	T	V	
121	S	S																			
118	S	S																			

FIGURE 40B

jb16

10 20 30 40 50 60
TAGATCTAGA CCACCATGGT TTTCACACCT CAGATACTAG GACTCATGCT CTTCTGGATT
70 80 90 100 110 120
TCAGCCTCCA GAGGTGAAAT TGTGCTAACT CAGTCTCCAG GCACCCTAAG CTTATCACCG

GGAGAAAGG

jb17

10 20 30 40 50 60
TAGACAGAAAT TCACCGTAC TTGATAAGTA GACGTGGAGC TTGTCCAGGT TTTTGTGGT
70 80 90 100 110 120
ACCAGTGTAG GTTGTGCTA ATACTTTGGC TGGCCCTGCA GGAAAGTGTGTA GCCCTTCTC

CCGGTGAT

jb18

10 20 30 40 50 60
AAGAGAATTC ACGCGTCCCC GTCCATCTCT GGAATACCCG ATAGGTTTCAG TGGCAGTGGA
70 80 90 100 110
TCAGGGACAG ATTCACCTCT CACAATAAGT AGGCTCGAGC CGGAAGATTT TGC

jb19

10 20 30 40 50 60
TAGATCTAGA GTTGAGAAGA CTACTTACGT TTTATTTCTA CCTTGGTCCC TTGTCCGAAC
70 80 90 100 110
GTATGAGGCC AACTGTTACT CTGTTGACAA TAATACACAG CAAAATCTTC CGGCTC

FIGURE 41A

jb20

10 20 30 40 50 60
TATATCTAGA CCACCATGGG ATGGAGCTGG ATCTTTCTCT TCCTCCTGTC AGGAACTGCA
70 80 90 100 110 120
GGTGTCCACT CTCAAGTCCA ACTGGTACAG TCTGGAGCTG AGGTTAAAAAA GCCTGGAAAGT
130
TCAGTAAGAG TTTC

jb21

10 20 30 40 50 60
TATATAGGTA CCACCATTGT AAGGATTAAT AAGTCCAACC CACTCAAGTC CTTTTCCAGG
70 80 90 100 110 120
TGCCTGTCTC ACCCAGTTCA TGGTATAACCC AGTGAATGAG TATCCGGAAG CTTTGCAGGA
130
AACTCTTACT GAAC

jb22

10 20 30 40 50 60
TATATAGGTA CCAGCTACAA CCAGAAGTTC AAGGGCACAG TTACAGTTC TTTGAAGCCT
70 80 90 100 110
TCATTTAACCC AGGCCTACAT GGAGCTCAGT AGTCTGTTT CTGAAGACAC TGCAGT

jb23

10 20 30 40 50 60
TATATCTAGA GGCCATTCTT ACCTGAGGAG ACGGTGACTA AGGTTCCCTG ACCCCAGTAG
70 80 90 100 110
TCCATAGAAT AGTCTCGAAA CCCCCGTCTT CTACAGTAAT AGACTGCAGT GTCTTC

FIGURE 41B

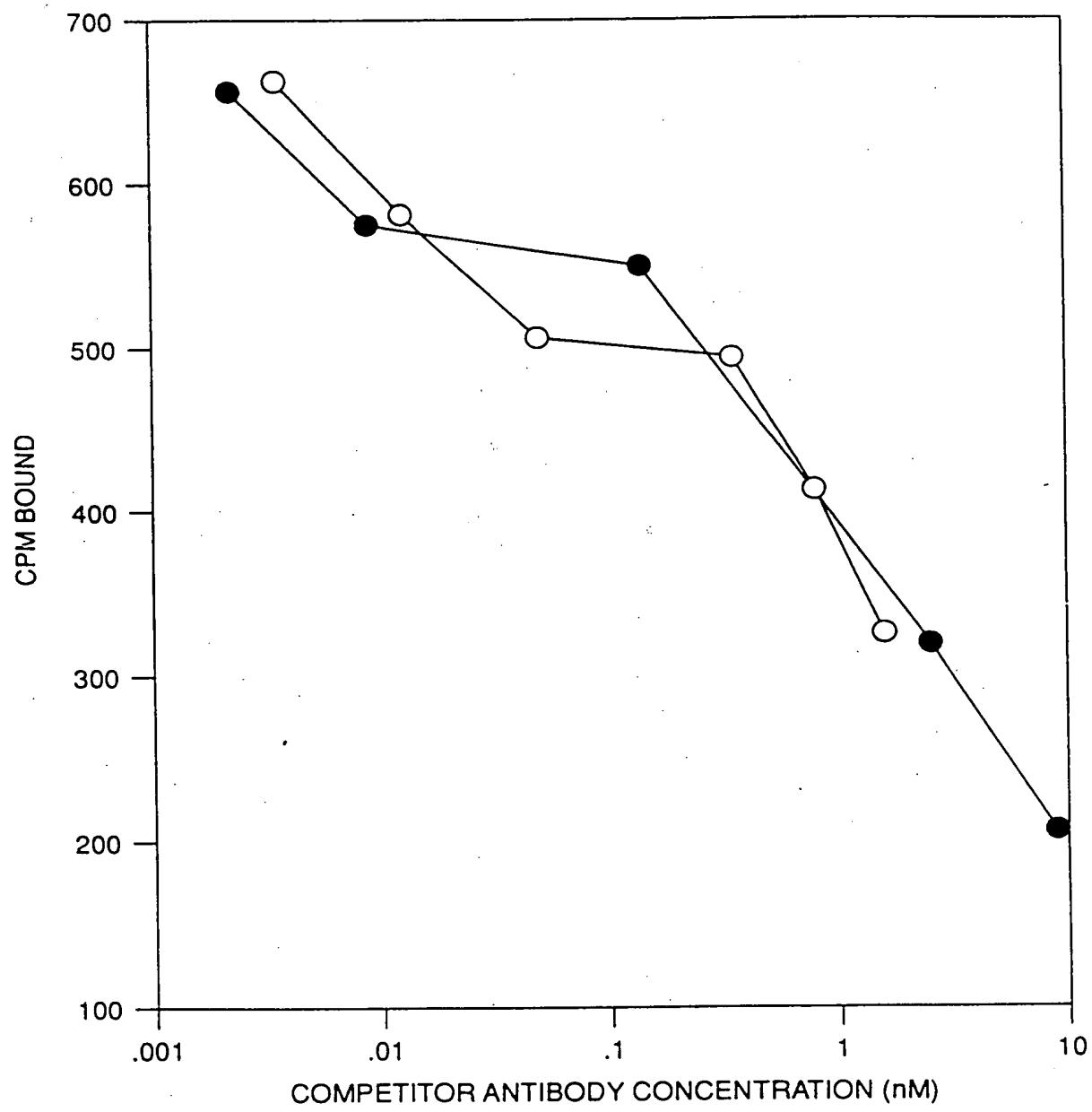


FIGURE 42

FIGURE 43A

FIGURE 43B

1	D	I	Q	M	T	Q	S	P	S	T	L	S	A	S	V	G	D	R	V	T
1	D	I	Q	M	T	Q	S	P	S	T	L	S	A	S	V	G	D	R	V	T
21	I	T	C	R	A	S	Q	S	I	N	T	W	L	A	W	Y	Q	Q	K	P
21	I	T	C	<u>K</u>	A	S	E	N	V	D	T	Y	V	S	W	Y	Q	Q	K	P
41	G	K	A	P	K	L	L	M	Y	K	A	S	S	L	E	S	G	V	P	S
41	G	K	A	P	K	L	L	<u>I</u>	Y	<u>G</u>	A	S	N	R	Y	T	G	V	P	S
61	R	F	I	G	S	G	S	G	T	E	F	T	L	T	I	S	S	L	Q	P
61	R	F	<u>S</u>	G	S	G	S	G	T	<u>D</u>	F	T	L	T	I	S	S	L	Q	P
81	D	D	F	A	T	Y	Y	C	Q	Q	Y	N	S	D	S	K	M	F	G	
81	D	D	F	A	T	Y	Y	C	<u>G</u>	<u>O</u>	S	Y	N	Y	P	F	T	F	G	
100	Q	G	T	K	V	E	V	K												
100	Q	G	T	K	V	E	V	K												

FIGURE 44A

1	Q	V	Q	L	V	Q	S	G	A	E	V	K	K	P	G	S	S	V	K	V
1	Q	V	Q	L	V	Q	S	G	A	E	V	K	K	P	G	S	S	V	K	V
21	S	C	K	A	S	G	G	T	F	S	R	S	A	I	I	W	V	R	Q	A
21	S	C	K	A	S	G	<u>Y</u>	<u>I</u>	<u>F</u>	<u>T</u>	<u>S</u>	<u>S</u>	<u>W</u>	<u>I</u>	<u>N</u>	<u>W</u>	<u>V</u>	<u>R</u>	<u>Q</u>	<u>A</u>
41	P	G	Q	G	L	E	W	M	G	G	I	V	P	M	F	G	P	P	N	Y
41	P	G	Q	G	L	E	W	M	G	<u>R</u>	<u>I</u>	<u>D</u>	<u>P</u>	<u>S</u>	<u>D</u>	<u>G</u>	<u>E</u>	<u>V</u>	<u>H</u>	<u>Y</u>
61	A	Q	K	F	Q	G	R	V	T	I	T	A	D	E	S	T	N	T	A	Y
61	<u>N</u>	<u>Q</u>	<u>D</u>	<u>F</u>	<u>K</u>	<u>D</u>	<u>R</u>	<u>V</u>	<u>T</u>	<u>I</u>	<u>T</u>	<u>A</u>	<u>D</u>	<u>E</u>	<u>S</u>	<u>T</u>	<u>N</u>	<u>T</u>	<u>A</u>	<u>Y</u>
81	M	E	L	S	S	L	R	S	E	D	T	A	F	Y	F	C	A	G	G	Y
81	M	E	L	S	S	L	R	S	E	D	T	A	<u>V</u>	<u>Y</u>	<u>Y</u>	<u>C</u>	<u>A</u>	<u>R</u>	<u>G</u>	<u>F</u>
101	G	I	Y	S	P	E	E	Y	N	G	G	L	V	T	V	S	S			
101	L	P	W	F	A	D	<u>W</u>	<u>G</u>	<u>O</u>	<u>G</u>	<u>T</u>	<u>L</u>	<u>V</u>	<u>T</u>	<u>V</u>	<u>S</u>	<u>S</u>			

FIGURE 44B

rh10

10	20	30	40	50	60
TTTTTTCTAG	ACCACCATGG	AGACCGATAAC	CCTCCTGCTA	TGGGTCTCC	TGCTATGGGT
70	80	90	100	110	
CCCAGGATCA	ACCGGAGATA	TTCAGATGAC	CCAGTCTCCG	TCGACCCTCT	CTGCT

rh11

10	20	30	40	50	60
TTTTAAGCTT	GGGAGCTTG	CCTGGCTCT	GCTGATACCA	GGATACATAA	GTATCCACAT
70	80	90	100	110	120
TTTCACTGGC	CTTGCAGGTT	ATGGTGACCC	TATCCCCGAC	GCTAGCAGAG	AGGTTCCACG

rh12

10	20	30	40	50	60
TTTTAAGCTT	CTAATTATG	GGGCATCCAA	CCGGTACACT	GGGGTACCTT	CACGCTTCAG
70	80	90	100	110	
TGGCAGTGGA	TCTGGGACCG	ATTCACCCCT	CACAATCAGC	TCTCTGCAGC	CAGATGAT

rh13

10	20	30	40	50	60
TTTTTTCTAG	AGCAAAAGTC	TACTTACGTT	TGACCTCCAC	CTTGGTCCCC	TGACCGAACG
70	80	90	100	110	120
TGAATGGATA	GTTGTAACTC	TGTCCGCAGT	AATAAGTGGC	GAAATCATCT	GGCTCCAGAG

FIGURE 45A

rh20

10	20	30	40	50	60
TTTTCTAGA	CCACCATGGG	ATGGAGCTGG	ATCTTCTCT	TCCTCCTGTC	AGGTACCGCG
70	80	90	100	110	
GGCGTGCACT	CTCAGGTCCA	GCTTGTCCAG	TCTGGGGCTG	AAGTCAAGAA	ACCT

rh21

10	20	30	40	50	60
TTTTGAATTC	TCGAGACCCT	GTCCAGGGGC	CTGCCTTACC	CAGTTTATCC	AGGAGCTAGT
70	80	90	100	110	120
AAAGATGTAG	CCAGAAGCTT	TGCAGGAGAC	CTTCACGGAG	CTCCCAGGTT	TCTTGACTTC

A

rh22

10	20	30	40	50	60
TTTTGAATTC	TCGAGTGGAT	GGGAAGGATT	GATCCTTCCG	ATGGTGAAGT	TCACTACAAT
70	80	90	100	110	120
CAAGATTCA	AGGACCGTGT	TACAATTACA	GCAGACGAAT	CCACCAATAAC	AGCCTACATG
130					
GAAC TGAGCA	GCCTGAG				

rh23

10	20	30	40	50	60
TTTTCTAGA	GGTTTAAGG	ACTCACCTGA	GGAGACTGTG	ACCAGGGTTC	CTTGGCCCCA
70	80	90	100	110	120
GTCAGCAAAC	CAGGGCAGAA	ATCCTCTTGC	ACAGTAATAG	ACTGCAGTGT	CCTCTGATCT
130					
CAGGCTGCTC	AGTT				

FIGURE 45B

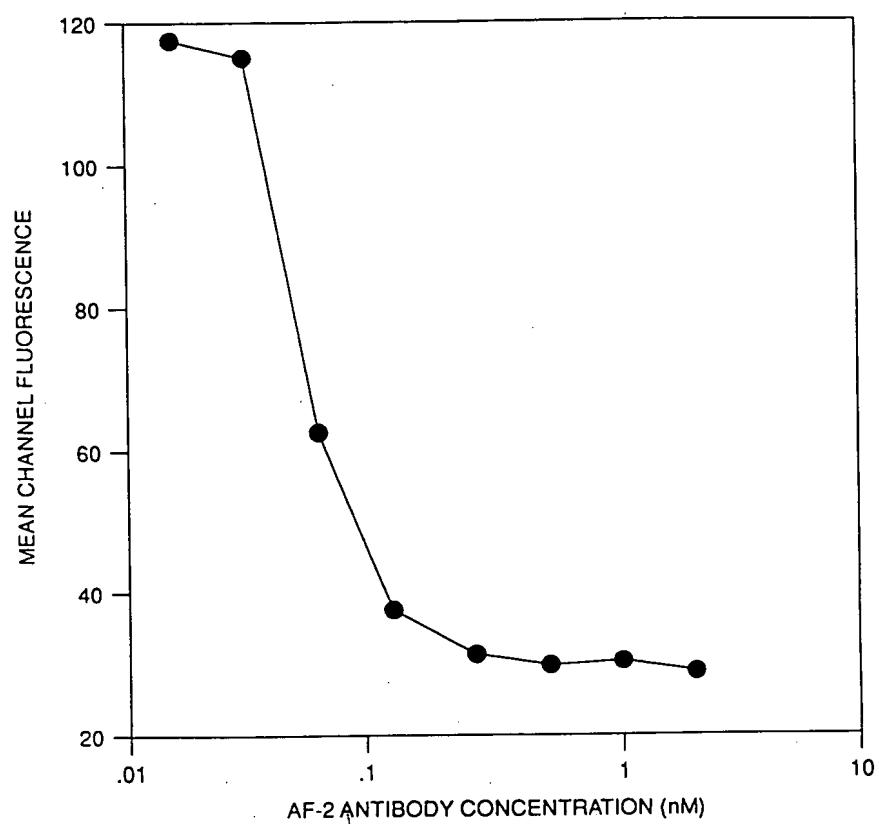


FIGURE 46